

79576

STIC-Biotech/ChemLib

Fr m: Chan, Christina
Sent: Wednesday, November 06, 2002 1:16 PM
To: Holleran, Anne; STIC-Biotech/ChemLib
Subject: RE: RUSH search for 09/480,977

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

-----Original Message-----

From: Holleran, Anne
Sent: Wednesday, November 06, 2002 9:52 AM
To: Chan, Christina
Subject: RUSH search for 09/480,977

Please approve and forward to STIC the following sequence search request. This case is an amendment due this biweek. Thanks.

Please search the following:

commercial and interference database search of SEQ ID NO: 4(aa)

Anne Holleran
AU: 1642
Tel: 308-8892
RM: 8e03

mailbox: 8e12

Searcher: H. Smith
Phone: _____
Location: _____
Date Picked Up: 11/7/02
Date Completed: 11/8/02
Searcher Prep/Review: 5
Clerical: _____
Online time: 5

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:10 : Search time 26 Seconds

(Without alignments)
312.722 Million cell updates/sec

Title: US-09-480-977-4

Perfect score: 277
Sequence: 1 HFKPCRDKLAYCLNDCECF.....SHKHCRCRCYGVRCDFL 47

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_minc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113.5	41.0	461	11	035947
2	111.5	40.3	298	11	09ES49
3	111.5	40.3	695	11	09ES80
4	104.5	37.7	241	6	007112
5	104.5	37.7	296	4	0961B3
6	102.5	37.0	111	11	09ES48
7	102.5	37.0	136	11	09ES47
8	102.5	37.0	256	11	09ES46
9	102.5	37.0	317	11	09ES43
10	102.5	37.0	323	11	09ES42
11	102.5	37.0	342	11	09ES41
12	102.5	37.0	700	11	09ES41
13	102.5	37.0	782	11	09ES41
14	99	35.7	89	11	09ES45
15	92.5	33.4	2192	5	001768
16	91.5	33.0	1213	13	090Y54

17	89	32.1	162	11	09ZOL5
18	89	32.1	1241	4	09UKK5
19	89	32.1	1241	4	09UKD4
20	89	32.1	1241	4	09BEV3
21	88	31.8	1239	11	P70628
22	87	31.4	217	5	09VVJ6
23	87	31.4	597	11	035727
24	85.5	30.9	1193	13	090819
25	85.5	30.9	1214	13	090YD2
26	85.5	30.9	1218	4	014902
27	85.5	30.9	1218	4	015122
28	85.5	30.9	1218	4	015122
29	85.5	30.9	1218	4	015122
30	84.5	30.5	1227	4	P78504
31	84.5	30.5	1218	11	09JUM4
32	84.5	30.5	1219	11	09QX00
33	83.5	30.1	127	12	0909F3
34	83	30.1	162	11	061521
35	83	30.0	861	11	09QW58
36	83	30.0	861	11	09QW58
37	82.5	29.8	862	11	09QW58
38	82.5	29.8	445	5	09W3W5
39	82.5	29.8	456	5	0961F3
40	81	29.2	264	5	020559
41	80.5	29.1	78	12	091736
42	80.5	29.1	125	12	041504
43	80.5	29.1	178	4	096F48
44	80.5	29.1	260	4	095898
45	80.5	29.1	530	4	096CW9
			1242	13	090Y57

ALIGNMENTS

RESULT 1	035947	PRELIMINARY:	PRT:	461 AA.
AC	035947			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	PRO-NEUREGULIN-1, ISOFORM ALPHA 2b PRECURSOR			
GN	NRG1 OR NDF			
OS	Mesocricetus auratus (Golden hamster)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA2B), AND SEQUENCE OF 64-81.			
RC	TISSUE-EMBRYO;			
RX	MEDLINE=98196966; PubMed=9537646;			
RA	Velasco J.A., Feljoo E., Avila M.A., Notario V.;			
RT	*Secretion of neu differentiation factor-like polypeptides by cph-			
RT	transformed fibroblasts: cloning and characterization of Syrian			
RT	hamster neurogulin cdnas *			
RL	Mol. Cell Biol. 21:156-163(1998).			
CC	-1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE			
CC	RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,			
CC	RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND			
CC	ACTIVATION OF THE ERBB RECEPTORS. MAY PLAY AN IMPORTANT ROLE IN			
CC	PROVIDING GROWTH ADVANTAGE IN NEOPLASTIC CELLS.			
CC	-1- SUBUNIT: THE CYTOPLASMIC DOMAIN INTERACTS WITH THE LIM DOMAIN			
CC	REGION OF LIMK1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: EXISTS AS TYPE I MEMBRANE PROTEIN AND AS A			
CC	PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-			
CC	BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).			
CC	-1- ALTERNATIVE PRODUCTS: DIFFERENT ISOFORMS ARE PRODUCED BY			
CC	ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ISOFORM			
CC	ALPHA2B/CLONE PM3.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED AT HIGHER LEVEL AFTER NEOPLASMIC			
CC	TRANSFORMATION OF CELLS.			
CC	-1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION			

OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
 CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
 CC DIMERIZATION (BY SIMILARITY).
 CC -1- DOMAIN: EBBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
 CC DOMAIN.
 CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
 CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
 CC FORM (BY SIMILARITY).
 CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES PROTEOLYTIC CLEAVAGE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
 CC EMBL: 096612; AAB71812.1; -
 CC HSSP: Q12784; IHRF.
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR003598; 19-C2.
 CC InterPro: IPR003006; 19-MHC.
 CC InterPro: IPR002154; Neuregulin.
 CC Pfam: PF00008; EGF; 1.
 CC Pfam: PF00047; 19; 1.
 CC Pfam: PF02158; Neuregulin; 1.
 CC PRINTS: PR01089; NEUREGULIN.
 CC SMART: SM00181; EGF; 1.
 CC SMART: SM00408; IGC2; 1.
 CC PROSITE: PS00022; EGF_1; UNKNOWN_1.
 CC PROSITE: PS0186; EGF_2; 1.
 CC PROSITE: PS0186; EGF_2; 1.
 CC Growth factor: EGF-like domain; Immunoglobulin domain; Glycoprotein;
 CC Transmembrane; Alternative splicing.
 CC PROPEP 1 13
 CC CHAIN 1 461
 CC CHAIN 14 241
 CC CHAIN 14 242
 CC TRANSMEM 243 265
 CC DOMAIN 266 461
 CC DOMAIN 50 119
 CC DOMAIN 165 177
 CC DOMAIN 178 222
 CC DISULFID 57 112
 CC DISULFID 182 196
 CC DISULFID 190 210
 CC DISULFID 212 221
 CC CARBOHYD 73 73
 CC CARBOHYD 120 120
 CC CARBOHYD 126 126
 CC CARBOHYD 164 164
 CC SEQUENCE 461 AA; 50890 MW; 935C9560E7148336 CRC64;
 Query Match 41.0%; Score 113.5; DB 11; Length 461;
 Best Local Similarity 34.8%; Pred. No. 1e-07;
 Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
 OY 1 HFKPCRDKLAVCLNDGCEVLETITGSHKH-CRCRKGYGVRCDQ 45
 Db 178 HLYKCAEKETFCVNGCEFTVKDLSNPSRYLCKQPGFTGARCIE 223
 RESULT 2
 OQESB9 PRELIMINARY; PRT; 298 AA.
 AC OQESB9
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SMDP NEUREGULIN ALPHA 2B (FRAGMENT).
 GN NR01.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BDX;

RA Carroll S.L., Anderson K.D., Frohner P.W.;
 RT "Structural and Functional Diversity of SMDP Neuregulin Splice
 RT Variants Expressed in the Adult Rat Nervous System."
 RT Submitted (OCT-1999) to the EMBL/Genbank/DBD databases.
 RL EMBL: AF194440; AAC28429.1; -
 DR EMBL: AF194440; AAC28429.1; -
 DR HSSP: Q12784; IHRF.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002154; Neuregulin.
 DR InterPro: IPR002114; PTS_HPR_ser.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF02158; Neuregulin; 1.
 DR PRINTS: PR01089; NEUREGULIN.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00001; EGF-like; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR NON_TER 1 1
 FT NON_TER 1 1
 FT SEQUENCE 298 AA; 32851 MW; BD76F014C3B33026 CRC64;
 Query Match 40.3%; Score 111.5; DB 11; Length 298;
 Best Local Similarity 34.8%; Pred. No. 1.3e-07;
 Matches 16; Conservative 13; Mismatches 16; Indels 1; Gaps 1;
 OY 1 HFKPCRDKLAVCLNDGCEVLETITGSHKH-CRCRKGYGVRCDQ 45
 Db 48 HLYKCAEKETFCVNGCEFTVKDLSNPSRYLCKQPGFTGARCIE 93
 RESULT 3
 OQESB0 PRELIMINARY; PRT; 695 AA.
 AC OQESB0
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SMDP NEUREGULIN ALPHA 2A.
 GN NR01.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BDX;
 RA Carroll S.L., Anderson K.D., Frohner P.W.;
 RT "Structural and Functional Diversity of SMDP Neuregulin Splice
 RT Variants Expressed in the Adult Rat Nervous System."
 RT Submitted (OCT-1999) to the EMBL/Genbank/DBD databases.
 RL EMBL: AF194439; AAC28428.1; -
 DR EMBL: AF194439; AAC28428.1; -
 DR HSSP: Q12784; IHRF.
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR002154; Neuregulin.
 DR InterPro: IPR002114; PTS_HPR_ser.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF02158; Neuregulin; 1.
 DR PRINTS: PR01089; NEUREGULIN.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00001; EGF-like; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR NON_TER 1 1
 FT NON_TER 1 1
 FT SEQUENCE 695 AA; 75646 MW; 5277F2CBA2FB6878 CRC64;
 Query Match 40.3%; Score 111.5; DB 11; Length 695;
 Best Local Similarity 34.8%; Pred. No. 3.1e-07;
 Matches 16; Conservative 13; Mismatches 16; Indels 1; Gaps 1;
 OY 1 HFKPCRDKLAVCLNDGCEVLETITGSHKH-CRCRKGYGVRCDQ 45
 Db 234 HLYKCAEKETFCVNGCEFTVKDLSNPSRYLCKQPGFTGARCIE 279
 RESULT 4

007112 ID 007112 PRELIMINARY; PRT: 241 AA.

AC 007112: PRELIMINARY; PRT: 241 AA.

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE NEUREGULIN-1, GLIAL GROWTH FACTOR 5 ISOFORM PRECURSOR (GGFBPP5).

GN NG1 OR GGF.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.

OC NCBI_TaxID=9913;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE-POSTERIOR PITUITARY;

RA MEDLINE-93205115; PubMed-8096067;

RA Marchionni M.A., Gooden A.D.J., Chen M.S., Bermingham-McDonogh O., Kirk C., Hendricks M., Danely F., Misumi D., Sudhalter J., Kobayashi K., Wroblewski D., Lynch C., Balasare M., Hiles I., Davis J.B., Huan J.J., Totty N.F., Olan M., McBurney R.N., Waterfield M.D., Stroobant P., Gwynne D.;

RA "Glial growth factors are alternatively spliced erb2 ligands expressed in the nervous system."

RT Nature 362:312-318(1993).

RL -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS, RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE ERBB RECEPTORS (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: SECRETED (PROBABLE).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS SYSTEM: SPINAL CORD AND BRAIN.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST FIVE DIFFERENT ISOFORMS: GGFBPP1, GGFBPP2, GGFBPP3, GGFBPP4 AND GGFBPP5 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC EMBL: L12259; AAA03540.1; -

DR HSSP: Q12784; IIRE.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR003598; Ig_C2.

DR InterPro: IPR003006; Ig_MHC.

DR Pfam: PF00008; EGF_1.

DR Pfam: PF00047; Ig_1.

DR SMART: SM00181; EGF_1.

DR SMART: SM00408; IGC2_1.

DR PROSITE: PS00022; EGF_1; UNKNOWN_1.

DR PROSITE: PS01186; EGF_2; FALSE_NEG.

KW Growth factor; EGF-like domain; Immunoglobulin domain; Alternative splicing.

FT PROPEP 1 19

FT CHAIN 20 241

FT DOMAIN 50 119

FT DOMAIN 165 177

FT DOMAIN 178 222

FT DISULFID 182 196

FT DISULFID 190 210

FT DISULFID 212 221

FT VARSPLIC 134 156

FT VARSPLIC 157 241

FT SEQUENCE 241 AA; 25955 MW; BF571297EBDA9796 CRC64;

Query Match

Best Local Similarity 37.7%; Score 104.5; DB 6; Length 241;

Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

OY 1 HFFPCBDKDLAYCLNDGCEVFIEITLGSKH-CRCKEGYGVRCDFL 47

DB 178 HLYKCAEKETFCVNGCECFVADLSNPSRYLCKPCNEFTGRCQNYV 225

RESULT 5

0961B3 ID 0961B3 PRELIMINARY; PRT: 296 AA.

AC 0961B3: PRELIMINARY; PRT: 296 AA.

DT 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE NEUREGULIN 1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN, AND NEUROBLASTOMA;

RA Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.

RL EMBL: BC007675; AAH07675.1; -

SO SEQUENCE 296 AA; 31699 MW; OF5C48C8465B6649 CRC64;

Query Match

Best Local Similarity 37.7%; Score 104.5; DB 4; Length 296;

Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

OY 1 HFFPCBDKDLAYCLNDGCEVFIEITLGSKH-CRCKEGYGVRCDFL 47

DB 233 HLYKCAEKETFCVNGCECFVADLSNPSRYLCKPCNEFTGRCQNYV 280

RESULT 6

09ESAB ID 09ESAB PRELIMINARY; PRT: 111 AA.

AC 09ESAB: PRELIMINARY; PRT: 111 AA.

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE SMD NEUREGULIN BETA 2 (FRAGMENT).

GN NG1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY;

RC TISSUE-AXOTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;

RA Carroll S.L., Anderson K.D., Frohnet P.W.;

RT "Structural and Functional Diversity of SMD Neuregulin Splice Variants Expressed in the Adult Rat Nervous System."

RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.

RL EMBL: AF194441; AAC28430.1; -

DR HSSP: Q12784; IIRE.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR00086; ER_target.

DR Pfam: PF00008; EGF_1.

DR SMART: SM00181; EGF_1.

DR SMART: SM00001; EGF-like; 1.

DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.

FT NON_TER 1 1

FT NON_TER 111 111

SO SEQUENCE 111 AA; 12198 MW; CC8BB870584C9F8C CRC64;

Query Match

Best Local Similarity 37.0%; Score 102.5; DB 11; Length 111;

Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFFPCBDKDLAYCLNDGCEVFIEITLGSKH-CRCKEGYGVRCDFL 47

DB 54 HLYKCAEKETFCVNGCECFVADLSNPSRYLCKPCNEFTGRCQNYV 101

RESULT 7

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O9ESA7 PRELIMINARY: PRT: 136 AA.
AC O9ESA7:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SMDP NEUREGULIN BETA 4 (FRAGMENT).
OS NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Carroll S.L., Anderson K.D., Fromert P.W.;
RT "Structural and Functional Diversity of SMDP Neuregulin Splice
RL Variants Expressed in the Adult Rat Nervous System.";
RL EMBL: AF194443; AAC28431.1; -
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR Pfam: PF00008; EGF_1.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF_1like; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 136 AA; 15235 MW; 116CBG91D6E8AEF5 CRC64;

Query Match
Best Local Similarity 37.0%; Score 102.5; DB 11; Length 136;
Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDRLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCDOFL 47
DB 54 HLKCAEKERTFCVNGGECFTVKDLSNPSRYLCKPCNEFTGDRCONVY 101

RESULT 8
O9ESA6 PRELIMINARY: PRT: 256 AA.
AC O9ESA6:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SMDP NEUREGULIN BETA 3 (FRAGMENT).
OS NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Carroll S.L., Anderson K.D., Fromert P.W.;
RT "Structural and Functional Diversity of SMDP Neuregulin Splice
RL Variants Expressed in the Adult Rat Nervous System.";
RL EMBL: AF194443; AAC28432.1; -
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR Pfam: PF00008; EGF_1.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF_1like; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
FT NON_TER 1
FT SEQUENCE 256 AA; 27335 MW; C8C08DEA68D33E39 CRC64;

Query Match
Best Local Similarity 37.0%; Score 102.5; DB 11; Length 256;
Matches 31.2%; Pred. No. 2e-06;

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Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDRLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCDOFL 47
DB 193 HLKCAEKERTFCVNGGECFTVKDLSNPSRYLCKPCNEFTGDRCONVY 240

RESULT 9
O9ESA3 PRELIMINARY: PRT: 317 AA.
AC O9ESA3:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GLIAL GROWTH FACTOR GGF BETA 2 (FRAGMENT).
OS NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Carroll S.L., Stonecypher M.S., Anderson K.D., Pearson R.J. Jr.;
RT "Structural and Functional Diversity of Glial Growth Factor Isoforms
RL Expressed in Regenerating Peripheral Nerve and Associated Neurons.";
RL EMBL: AF194995; AAC28449.1; -
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000886; ER_target.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF_1like; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00408; IgC2; 1.
DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
KW Immunoglobulin domain.
FT NON_TER 1
FT SEQUENCE 317 AA; 34785 MW; 4487FA3E9CD876B9 CRC64;

Query Match
Best Local Similarity 37.0%; Score 102.5; DB 11; Length 317;
Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDRLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCDOFL 47
DB 260 HLKCAEKERTFCVNGGECFTVKDLSNPSRYLCKPCNEFTGDRCONVY 307

RESULT 10
O9ESA2 PRELIMINARY: PRT: 323 AA.
AC O9ESA2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GLIAL GROWTH FACTOR GGF BETA 3 (FRAGMENT).
OS NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Carroll S.L., Stonecypher M.S., Anderson K.D., Pearson R.J. Jr.;

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RA Frohner P.W.;
RT *Structural and Functional Diversity of Glial Growth Factor Isoforms
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF194996; AAG28450.1;
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003599; IG_c2.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003600; IG_c2.
DR InterPro: IPR003066; IG_MHC.
DR Pfam: PF00047; IG_1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00409; IG_1.
DR SMART: SM00408; IG_c2; 1.
DR SMART: SM00410; IG-like; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 323 AA; 35358 MW; C7DF153A939A80C8 CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 323;
Best Local Similarity 31.2%; Pred. No. 2.5e-06;
Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDKLAVCLNDGCEVFIEITLNGSHKH-CRCKEGYGVRCDOFL 47
DB 260 HLKCAEKETFCVNGCEFTVKDLSNPSRYLCKCPNEFTGDRCONVY 307

RESULT 11
OQESAL PRELIMINARY; PRT; 342 AA.
AC OQESAL:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLIAL GROWTH FACTOR GGF BETA 4 (FRAGMENT).
GN NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RC TISSUE-AXOTOMIZED LUMBAR DORSAL ROOT GANGLION/SPINAL CORD;
RA Carroll S.L., Stonecypher M.S., Anderson K.D., Pearson R.J. Jr.,
RA Frohner P.W.;
RT *Structural and Functional Diversity of Glial Growth Factor Isoforms
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF194997; AAG28451.1;
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR003599; IG_c2.
DR InterPro: IPR003598; IG_c2.
DR InterPro: IPR003066; IG_MHC.
DR Pfam: PF00047; IG_1.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF-like; 1.
DR SMART: SM00409; IG_1.
DR SMART: SM00408; IG_c2; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
KW Immunoglobulin domain.
FT NON_TER 1
SQ SEQUENCE 342 AA; 37836 MW; 8BE36FC83653124 CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 342;
Best Local Similarity 31.2%; Pred. No. 2.7e-06;
Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
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OY 1 HFKPCRDKLAVCLNDGCEVFIEITLNGSHKH-CRCKEGYGVRCDOFL 47
DB 260 HLKCAEKETFCVNGCEFTVKDLSNPSRYLCKCPNEFTGDRCONVY 307

RESULT 12
OQESB1 PRELIMINARY; PRT; 700 AA.
AC OQESB1:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SMDF NEUREGULIN BETA 1A.
GN NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RA Carroll S.L., Anderson K.D., Frohner P.W.;
RT *Structural and Functional Diversity of SMDF Neuregulin Splice
RL Submitted (OCT-1999) to the Adult Rat Nervous System.
DR EMBL: AF194438; AAG28427.1;
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002114; PTS_HPR_ser.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF02158; Neuregulin; 1.
DR PRINTS: PR01089; NEUREGULIN.
DR SMART: SM00181; EGF_1.
DR SMART: SM00001; EGF-like; 1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
SQ SEQUENCE 700 AA; 76386 MW; 2F811B17ECC49DA CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 700;
Best Local Similarity 31.2%; Pred. No. 5.7e-06;
Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDKLAVCLNDGCEVFIEITLNGSHKH-CRCKEGYGVRCDOFL 47
DB 234 HLKCAEKETFCVNGCEFTVKDLSNPSRYLCKCPNEFTGDRCONVY 281

RESULT 13
OQESAS PRELIMINARY; PRT; 782 AA.
AC OQESAS:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLIAL GROWTH FACTOR BETA 1A (FRAGMENT).
GN NRGI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE-SPINAL CORD/BRAIN STEM;
RA Carroll S.L., Stonecypher M.S., Anderson K.D., Pearson R.J. Jr.,
RA Frohner P.W.;
RT *Structural and Functional Diversity of Glial Growth Factor Isoforms
RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF194993; AAG28433.1;
DR HSSP: Q12784; 1HRE.
DR InterPro: IPR000561; EGF-like.
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DR InterPro: IPR003599; IG_C2.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR002154; Neuregulin.
 DR InterPro: IPR002114; PTS_HPR_ser.
 DR Pfam: PF00047; 1g; 1.
 DR Pfam: PF02158; Neuregulin; 1.
 DR PRINTS: PR01089; NEUREGULIN.
 DR SMART: SM00181; EGF_1.
 DR SMART: SM00001; EGF_Like; 1.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR Immunoglobulin domain; 1.
 FT NON_TER 1
 SQ SEQUENCE 782 AA; 86036 MW; F6174A68F4E27BDE CRC64;

Query Match 37.0%; Score 102.5; DB 11; Length 782;
 Best Local Similarity 31.2%; Pred. No. 6,5e-06;
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFKPCRDALVCLNDECFYETLTGSHKH-CRCKEGYGVRCQDPL 47
 -DB 316 HLICAEKERTCVNGCECTVNDLNSPRLVLCRPNETGDRCONV 363

RESULT 14
 ID 091M20 PRELIMINARY; PRT; 89 AA.
 AC 091M20;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE LSDV016 EGF-LIKE GROWTH FACTOR.
 GN LSDV016.
 OS Jumpy skin disease virus.
 OC Viruses: dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Capripoxvirus.
 OK NCBI_TaxID=59509;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-NETHLING 2490;
 RX MEDLINE-21329495; PubMed-11435593;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RT "Genome of Jumpy skin disease virus";
 RL J. Virol. 75:7122-7130(2001).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-NETHLING 2490;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF325528; AAK8497.1;
 SQ SEQUENCE 89 AA; 10646 MW; 1D5F3FD7D06174E0 CRC64;

Query Match 35.7%; Score 99; DB 12; Length 89;
 Best Local Similarity 43.9%; Pred. No. 2e-06;
 Matches 18; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

OY 7 DKDLAVCLNDECFYETLTGSHKH-CRCKEGYGVRC 43
 -DB 40 DKSINCLNGGTCYRTTFLSYNKRPLMFCRCKLGEYGVRC 80

RESULT 15
 ID 001768 PRELIMINARY; PRT; 2192 AA.
 AC 001768;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 242.7 KDA PROTEIN.
 GN T21E3.3.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Telodoridae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE-99069613; PubMed-9851916;
 RA None;
 RT "Investigating biology. The C. elegans Sequencing Consortium";
 RL Science 282:2012-2018(1998).
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z., Le T.T.;
 RT "The sequence of C. elegans cosmid T21E3";
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 RN 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003133; AAB54138.2;
 DR HSSP: Q07954; 1CR8.
 DR InterPro: IPR000561; EGF_Like.
 DR InterPro: IPR002049; Laminin_EGF.
 DR InterPro: IPR000033; Ldl_receptor_rep.
 DR InterPro: IPR002172; Ldl_receptor_A.
 DR Pfam: PF00008; EGF; 8.
 DR Pfam: PF00057; Ldl_receptor_a; 18.
 DR Pfam: PF00058; Ldl_receptor_b; 8.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR PRINTS: PR00261; LDLRECEPTOR.
 DR SMART: SM00181; EGF; 23.
 DR SMART: SM00192; LDLA; 18.
 DR SMART: SM00135; LY; 7.
 DR PROSITE: PS00022; EGF_1; UNKNOWN_9.
 DR PROSITE: PS01186; EGF_2; 7.
 DR PROSITE: PS01209; LDLRA_1; 10.
 DR PROSITE: PS00068; LDLRA_2; 12.
 KW EGF-like domain; Glycoprotein; Hypothetical protein.
 SQ SEQUENCE 2192 AA; 242666 MW; F4762A5EBCA45BDA CRC64;

Query Match 33.4%; Score 92.5; DB 5; Length 2192;
 Best Local Similarity 42.9%; Pred. No. 0.00049;
 Matches 18; Conservative 8; Mismatches 7; Indels 9; Gaps 3;

OY 5 CRDKDLAVCLNDECFYETLTGSHKHCRCKEGYGVRCQD 45
 -DB 1918 CDD-----YCTNNSRC-----TITNGTHPECDCKPQFKLRCEQ 1951

Search completed: November 7, 2002, 10:02:59
 Job time : 27 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:08 ; Search time 11 seconds

(without alignments)
165 438 Million cell updates/sec

Title: US-09-480-977-4

Sequence: 1 HRPCKDKLAVCLNDGECF.....SHKHCRCRKGVGVRDQFL 47

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	100.0	713	NRG3_MOUSE	035181 mus musculus
2	277	100.0	720	NRG3_HUMAN	P56975 homo sapien
3	126.5	45.7	677	NRG1_XENLA	O93383 xenopus lae
4	113.5	41.0	639	NRG1_HUMAN	O02297 h. pro-neure
5	110	39.7	115	NRG4_MOUSE	O94744 mus musculus
6	104.5	37.7	296	SMDE_HUMAN	O14971 homo sapien
7	104	37.5	756	NRG2_MOUSE	P56974 mus musculus
8	102.5	37.0	662	NRG1_RAT	P43322 r. pro-neure
9	98.5	35.6	602	NRG1_CHICK	O14511 homo sapien
10	90	32.5	850	NRG2_HUMAN	O35569 ratius norv
11	90	32.5	868	NRG2_MOUSE	O19444 homo sapien
12	89.5	32.3	169	EREG_HUMAN	P08441 shope fibro
13	85	30.7	80	GRFA_SFYKA	O01705 mus musculus
14	83	30.0	2531	NRG1_MOUSE	O05928 mus musculus
15	82.5	29.8	177	BTC_MOUSE	O94744 mus musculus
16	82.5	29.8	177	BTC_BOVIN	O05928 mus musculus
17	82	29.6	85	GRFA_MYXVL	O94744 mus musculus
18	82	29.6	230	SPT_DROME	O01083 drosophila
19	80.5	29.1	125	V211_FOWPY	O94744 mus musculus
20	80.5	29.1	178	BTC_HUMAN	P35070 homo sapien
21	79.5	28.7	140	GRFA_VACCV	P01136 vacclia vi
22	79.5	28.7	142	GRFA_VACCC	P20494 vacclia vi
23	79.5	28.7	159	TGFA_MOUSE	P48030 mus musculus
24	79.5	28.7	159	TGFA_MOUSE	P01134 ratius norv
25	79	28.5	2531	NRG1_RAT	O07008 ratius norv
26	78	28.2	1207	BGF_HUMAN	P01133 homo sapien
27	77.5	28.0	714	DL1_RAT	P97677 ratius norv
28	77.5	28.0	722	DL1_MOUSE	O61483 mus musculus
29	76	27.4	484	LEM2_PIG	P98110 sus scrofa
30	76	27.4	1217	EGF_MOUSE	P01132 sus muscu
31	76	27.4	2139	CRB_DROME	P10040 drosophila
32	75	27.1	611	LEM2_CANPA	P33730 canis fami
33	74.5	26.9	603	FM12_CANVO	O04962 cavia porce

34	74.5	26.9	723	1	DL1_HUMAN	O00548 homo sapien
35	74.5	26.9	1429	1	LI12_CABEL	P14385 caenorhabd
36	74	26.7	551	1	LEM2_RABIT	P27113 oryctolagus
37	74	26.7	610	1	LEM2_HUMAN	P16581 homo sapien
38	74	26.7	2871	1	FBN1_BOVIN	P98133 bos taurus
39	74	26.7	2871	1	FBN1_HUMAN	P35555 homo sapien
40	74	26.7	2871	1	FBN1_MOUSE	O61554 mus musculus
41	74	26.7	2871	1	FBN1_PIG	O94736 sus scrofa
42	73	26.4	294	1	GRK_DROME	P42287 drosophila
43	73	26.4	409	1	MGFN_MOUSE	P79385 sus scrofa
44	73	26.4	1964	1	NTC4_MOUSE	P31695 mus musculus
45	73	26.4	2524	1	NOTC_XENLA	P21783 xenopus lae

ALIGNMENTS

RESULT 1	NRG3_MOUSE	STANDARD	PRT	713 AA.
AC	NRG3_MOUSE			
AC	035181:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Pro-neuregulin-3 precursor (Pro-NRG3) [Contains: Neuregulin-3 (NRG-3)]			
DE	NRG3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97420720: PubMed=9275162;			
RA	Zhang D., Sliwkowski M.X., Matk M., Frantz G., Akita R., Sun Y.,			
RA	Hillan K., Crowley C., Brush J., Godowski P.J.;			
RT	Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that			
RT	binds and activates ErbB4.*			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).			
RL	-1- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR.			
CC	-1- BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND			
CC	ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR,			
CC	ERBB2 OR ERBB3 RECEPTORS.			
CC	-1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS			
CC	A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE			
CC	MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN SYMPATHETIC, MOTOR, AND SENSORY			
CC	NEURONS.			
CC	-1- DEVELOPMENTAL STAGE: DETECTED AS EARLY AS E11. IN E13 EMBRYOS,			
CC	DETECTED MAINLY IN THE NERVOUS SYSTEM. IN E16 EMBRYOS, DETECTED IN			
CC	THE BRAIN, SPINAL CORD, TRIGEMINAL, VESTIBULAR-COCHLEAR, AND			
CC	SPINAL GANGLIA. IN ADULTS, EXPRESSED IN SPINAL CORD, AND NUMEROUS			
CC	BRAIN REGIONS.			
CC	-1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION			
CC	OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE			
CC	PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN			
CC	DIMERIZATION (BY SIMILARITY).			
CC	-1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE			
CC	DOMAIN (BY SIMILARITY).			
CC	-1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE			
CC	EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR			
CC	FORM (BY SIMILARITY).			
CC	-1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY			
CC	SIMILARITY).			
CC	-1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
CC	-1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

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CC EMBL: AF010130; AB070914.1; ..

CC MGI: MGI:1097165; Nr93.

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR002154; Neuregulin.

DR Pfam: PF00008; EGF_1.

DR Pfam: PF02158; Neuregulin; 1.

DR SMART: SM00181; EGF_1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 1.

KW Growth factor; EGF-like domain; Transmembrane; Multigene family.

FT CHAIN 1 713 PRO-NEUREGULIN-3, MEMBRANE-BOUND FORM.

FT CHAIN 1 361 NEUREGULIN-3

FT DOMAIN 1 362 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 363 383 INTERNAL SIGNAL SEQUENCE (POTENTIAL).

FT DOMAIN 384 713 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 105 287 SER/THR-RICH.

FT DOMAIN 288 331 EGF-LIKE.

FT DOMAIN 13 21 POLY-ALA.

FT DOMAIN 26 34 POLY-ALA.

FT DOMAIN 127 135 POLY-THR.

FT DOMAIN 250 253 POLY-ALA.

FT DOMAIN 254 263 POLY-SER.

FT DOMAIN 264 267 POLY-SER.

FT DISULFID 292 306 BY SIMILARITY.

FT DISULFID 300 319 BY SIMILARITY.

FT DISULFID 321 330 BY SIMILARITY.

SO SEQUENCE 713 AA; 77369 MW; 9E7DD5E7FC8DC60 CRC64;

Query Match 100.0%; Score 277; DB 1; Length 713;

Best Local Similarity 100.0%; Pred. No. 5.9e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDKLAYCLNDECFYETLTGSHKCRCKEGYGVRCDFL 47

DB 288 HFKPCRDKLAYCLNDECFYETLTGSHKCRCKEGYGVRCDFL 334

RESULT 2

NRG3_HUMAN STANDARD; PRT; 720 AA.

AC P56975;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Pro-neuregulin-3 precursor (Pro-NRG3) [Contains: Neuregulin-3 (NRG-3)].

GN NRG3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

XP [1]

RP SEQUENCE FROM N.A.

RX TISSUE-Fetal brain;

RX MEDLINE-97420720; PubMed-9275162;

RA Zhang D., Sliwkowski M.X., Frantz G., Akita R., Sun Y., Hillen K., Crowley C., Brush J., Godowski P.J.;

RT "Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that binds and activates ErbB4";

RL Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997)

CC -1- FUNCTION: DIRECT LIGAND FOR THE ERBB4 TYROSINE KINASE RECEPTOR. BINDING RESULTS IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND ACTIVATION OF THE RECEPTOR. DOES NOT BIND TO THE EGF RECEPTOR.

CC ERBB2 OR ERBB3 RECEPTORS.

CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN MOST REGIONS OF THE BRAIN WITH THE EXCEPTION OF CORPUS CALLOSUM. EXPRESSED AT LOWER LEVEL IN TESTIS. NOT DETECTED IN HEART, PLACENTA, LUNG, LIVER, SKELETAL

MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, OVARY, SMALL INTESTINE, COLON AND PERIPHERAL BLOOD LEUCOCYTES.

CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).

CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).

CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR FORM (BY SIMILARITY).

CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

DR MIM: 605533; ..

DR InterPro: IPR000561; EGF-like.

DR InterPro: IPR002154; Neuregulin.

DR Pfam: PF02158; Neuregulin; 1.

DR SMART: SM00181; EGF_1.

DR PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF_2; 1.

KW Growth factor; EGF-like domain; Transmembrane; Multigene family.

FT CHAIN 1 720 PRO-NEUREGULIN-3, MEMBRANE-BOUND FORM.

FT CHAIN 1 359 NEUREGULIN-3.

FT DOMAIN 1 360 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 361 381 INTERNAL SIGNAL SEQUENCE (POTENTIAL).

FT DOMAIN 382 720 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 105 285 SER/THR-RICH.

FT DOMAIN 286 329 EGF-LIKE.

FT DOMAIN 5 8 POLY-ALA.

FT DOMAIN 13 21 POLY-ALA.

FT DOMAIN 26 34 POLY-ALA.

FT DOMAIN 127 135 POLY-THR.

FT DOMAIN 252 260 POLY-SER.

FT DOMAIN 262 265 POLY-SER.

FT DISULFID 290 304 BY SIMILARITY.

FT DISULFID 298 317 BY SIMILARITY.

FT DISULFID 319 328 BY SIMILARITY.

SO SEQUENCE 720 AA; 77900 MW; A46F10DD895A693 CRC64;

Query Match 100.0%; Score 277; DB 1; Length 720;

Best Local Similarity 100.0%; Pred. No. 5.9e-26;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDKLAYCLNDECFYETLTGSHKCRCKEGYGVRCDFL 47

DB 286 HFKPCRDKLAYCLNDECFYETLTGSHKCRCKEGYGVRCDFL 332

RESULT 3

NRG1_XENLA STANDARD; PRT; 677 AA.

AC O93853; O946N0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1].

GN NRG1.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

XP [1]

RP SEQUENCE FROM N.A. (ISOFORM ALPHA1), AND ALTERNATIVE SPLICING.

RX MEDLINE-98352126; PubMed-9685585;

RA Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., Tsai K.W.K.;

RT "Cloning of cDNAs encoding xenopus neuregulin: expression in myotomal muscle during embryo development";

RL Brain Res. Mol. Brain Res. 58:59-73(1998).

CC [2]

SO SEQUENCE FROM N.A. (ISOFORM CRD).

RA Kirk C., Hendricks M., Danely F., Misumi D., Sudhalter J.,
 RA Kobayashi K., Wroblewski D., Lynch C., Baldassarre M., Hiles I.,
 RA Davis J.B., Hsuan J.J., Totty N.F., Otsu M., McBurey R.N.,
 RA Waterfield M.D., Stroobant P., Gwynne D.,
 RT Galil growth factors are alternatively spliced erbB2 ligands
 RT expressed in the nervous system.";
 RL Nature 362:312-318(1993).
 [15]
 RP SEQUENCE FROM N.A. OF GAMMA-HEREGULIN FUSION PROTEIN.
 RC TISSUE-BREAST CANCER;
 RA MEDLINE-97472144; PubMed-9333014;
 RA Schneider G., Fitzpatrick V.D., Sliwkowski M.X.;
 RT Gamma-hergulin: a novel heregulin isoform that is an autocrine
 RT growth factor for the human breast cancer cell line, MDA-MB-175.";
 RL Oncogene 15:1385-1394(1997).
 [16]
 RP SEQUENCE OF 1-210 FROM N.A.
 RA Schoumacher F., Herzer S., Flury N., Kueng W., Mueller H.,
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.
 [17]
 RP SEQUENCE OF 19-27
 RA MEDLINE-93366731; PubMed-7689552;
 RA Culuscu J., M., Plozman G.D., Carlton G.W., Green J.M., Shoyab M.;
 RT Characterization of a breast cancer cell differentiation factor that
 RT specifically activates the HER4/p180erbB4 receptor.";
 RL J. Biol. Chem. 268:18407-18410(1993).
 [18]
 RP CHROMOSOMAL TRANSLOCATION.
 RA MEDLINE-99455251; PubMed-10523851;
 RA Wang X.-Z., Jolicoeur E.M., Conte N., Chafanet M., Zhang Y.,
 RT Mozziconacci M.-J., Felner H., Birnbaum D., Pepusque M.-J., Ron D.;
 RT Gamma-hergulin is the product of a chromosomal translocation fusing
 RT the DCC4 and HGL/NRG1 genes in the MDA-MB-175 breast cancer cell
 RT line.";
 RL Oncogene 18:5718-5721(1999).
 [19]
 RP CHROMOSOMAL TRANSLOCATION.
 RA MEDLINE-20065180; PubMed-10597312;
 RA Liu X., Baker E., Eyre H.J., Sutherland G.R., Zhou M.;
 RT Gamma-hergulin: a fusion gene of DCC-4 and neuregulin-1 derived from
 RT a chromosome translocation.";
 RL Oncogene 18:7110-7114(1999).
 [110]
 RP STRUCTURE BY NMR OF 175-241 (ISOFORM ALPHA).
 RA MEDLINE-94341264; PubMed-8062828;
 RA Nagata K., Kohda D., Hatanaka H., Ichikawa S., Matsuda S.,
 RT Yamamoto T., Suzuki A., Inagaki F.;
 RT Solution structure of the epidermal growth factor-like domain of
 RT heregulin-alpha, a ligand for p180erbB-4.";
 RL EMBL J. 13:3517-3523(1994).
 -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE
 RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,
 RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
 ACTIVATION OF THE ERBB RECEPTORS. THE MULTIPLE ISOFORMS PERFORM
 DIVERSE FUNCTIONS SUCH AS INDUCING GROWTH AND DIFFERENTIATION OF
 EPITHELIAL, GLIAL, NEURONAL, AND SKELETAL MUSCLE CELLS; INDUCING
 EXPRESSION OF ACETYLCHOLINE RECEPTOR IN SYNAPTIC VESICLES DURING
 LOBULOALVEOLAR BUDDING AND MILK PRODUCTION IN THE MAMMARY GLAND
 AND INDUCING DIFFERENTIATION OF MAMMARY TUMOR CELLS; STIMULATING
 SCHWANN CELL PROLIFERATION; IMPLICATION IN THE DEVELOPMENT OF THE
 MYOCARDIUM SUCH AS TRABECULATION OF THE DEVELOPING HEART.
 -1- SUBUNIT: THE CYTOPLASMIC DOMAIN INTERACTS WITH THE LIM DOMAIN
 REGION OF LIMK1 (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
 A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
 MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE. THE SECRETED
 ISOFORM GGF2 HAS A SIGNAL PEPTIDE. THE ISOFORM BETA3 MAY BE
 NUCLEAR.
 -1- ALTERNATIVE PRODUCTS: AT LEAST 10 ISOFORMS: ALPHA (SHOWN HERE);
 ALPHA1A, ALPHA2B, ALPHA3A, BETA1, BETA1A, BETA2, BETA3/GGFHBL,
 GGF2/GGFHP2 AND SMDP (AC Q15491); ARE PRODUCED BY ALTERNATIVE

CC SPLICING. THEY HAVE BEEN CLASSIFIED AS TYPE I NRGS (VARIANTS WITH
 CC AN IG DOMAIN AND A GLYCOSYLATION DOMAIN; ALPHA AND BETA), TYPE II
 CC NRGS (VARIANTS WITH AN IG DOMAIN BUT NO GLYCOSYLATION DOMAIN;
 CC GGF2) AND TYPE III NRGS (VARIANTS WITH A CYS-RICH DOMAIN; SMDP).
 CC ALL THESE ISOFORMS PERFORM DISTINCT TISSUE-SPECIFIC FUNCTIONS.
 CC -1- TISSUE SPECIFICITY: TYPE I ISOFORMS ARE THE PREDOMINANT FORMS
 CC EXPRESSED IN THE ENDOCARDIUM. ISOFORM ALPHA IS EXPRESSED IN
 CC BREAST, OVARY, TESTIS, PROSTATE, HEART, SKELETAL MUSCLE, LUNG,
 CC BUT NOT IN UTERUS, STOMACH, PANCREAS, AND SPLEEN. ALPHA2 IS THE
 CC PREDOMINANT FORM IN MESENCHYMAL CELLS AND IN NONNEURONAL ORGANS,
 CC WHEREAS BETA1 IS THE MAJOR NEURONAL FORM. BETA3 IS EXPRESSED IN
 CC SPINAL CORD AND BRAIN. GGF2 IS THE MAJOR FORM IN SKELETAL MUSCLE
 CC CELLS; IN THE NERVOUS SYSTEM IT IS EXPRESSED IN SPINAL CORD AND
 CC BRAIN. ALSO DETECTED IN ADULT HEART, PLACENTA, LUNG, LIVER,
 CC KIDNEY, AND PANCREAS.
 CC -1- DEVELOPMENTAL STAGE: DETECTABLE AT EARLY EMBRYONIC AGES.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
 CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
 CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
 CC DIMERIZATION (BY SIMILARITY).
 CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
 CC DOMAIN.
 CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
 CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
 CC FORM.
 CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
 CC SIMILARITY).
 CC -1- DISEASE: INVOLVED IN A RARE T(8;11) CHROMOSOMAL TRANSLOCATION THAT
 CC FUSES THE 5' END OF DCC4 TO NRG1 (ISOFORM BETA3). THE PRODUCT OF
 CC THIS TRANSLOCATION HAS FIRST BE THOUGHT TO BE AN ALTERNATIVE
 CC SPLICED ISOFORM, CALLED GAMMA-HEREGULIN. GAMMA-HEREGULIN IS A
 CC SOLUBLE ACTIVATING LIGAND FOR THE ERBB2-ERBB3 RECEPTOR COMPLEX AND
 CC ACTS AS AN AUTOCRINE GROWTH FACTOR IN A SPECIFIC BREAST CANCER
 CC CELL LINE (MDA-MB-175). NOT DETECTED IN BREAST CARCINOMA SAMPLES,
 CC INCLUDING DUCTAL, LOBULAR, MEDULLARY, AND MUCINOUS HISTOLOGICAL
 CC TYPES. NEITHER IN OTHER BREAST CANCER CELL LINES.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
 CC -1- THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb.ch).
 CC -----
 CC EMBL: M94165; AAAS8638.1;
 CC EMBL: M94166; AAAS8639.1;
 CC EMBL: M94167; AAAS8640.1;
 CC EMBL: M94168; AAAS8641.1;
 CC EMBL: L12261; AAB59358.1;
 CC EMBL: U02325; AAB19950.1;
 CC EMBL: U02326; AAB19951.1;
 CC EMBL: U02327; AAB19952.1;
 CC EMBL: U02328; AAB19953.1;
 CC EMBL: U02329; AAB19954.1;
 CC EMBL: U02330; AAB19955.1;
 CC EMBL: L12260; AAB59622.1;
 CC EMBL: AF026146; AAD01795.1;
 CC EMBL: AF009227; AAC51756.1; ALT_INIT.
 CC PDB: 1HRE; 15-OCT-94.
 CC PDB: 1HRP; 15-OCT-94.
 CC PDB: 142445;
 CC InterPro: IPR000561; EGF-like.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR002154; Neuregulin.
 CC Pfam: PF00047; 1g.1.
 CC Pfam: PF02158; Neuregulin; 1.
 CC PRINTS: PR01089; NEUREGULIN.
 CC PROSITE: PS00022; EGF_1; 1.

DR PROSITE: PS01186; EGF-2.1.
 KW Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
 KW Transmembrane; Multigene family; Polymorphism; 3D-structure;
 KW Alternative splicing; Chromosomal translocation.

Query Match 41.0%; Score 113.5; DB 1; Length 639;
 Best Local Similarity 34.8%; Pred. No. 2.3e-06;
 Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

OY 1 HEPGDRDLAYCNDGECVETLTGSHKH-CRCKEGYGRCDQ 45
 DB 177 HLYKCAKEKTEFCVNGSECFMKDLSNPSRYLCKRCQPFETARCTE 222

RESULT 5
 NR04_MOUSE STANDARD: PRT; 115 AA.
 AC 09WTK4;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Pro-neuregulin-4, short isoform (Pro-NRG4) [Contains: Neuregulin-4 (NRG-4)].
 GN NRG4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99276096; PubMed=10348342;
 RA Harari D., Zahar E., Romano J., Shelly M., Pierce J.H., Andrews G.C.,
 RT Yarden Y.: a novel growth factor that acts through the ErbB-4
 receptor tyrosine kinase.
 RL Oncogene 18:2681-2689(1999).
 CC -1- FUNCTION: LOW AFFINITY LIGAND FOR THE ERBB4 TYROSINE KINASE
 RECEPTOR. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,
 RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
 ACTIVATION OF THE ERBB RECEPTORS. DOES NOT BIND TO THE ERBB1,
 ERBB2 AND ERBB3 RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
 A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
 MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS MAY BE PRODUCED BY
 ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PANCREAS; WEAKLY EXPRESSED
 IN MUSCLE.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
 OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
 PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
 DIMERIZATION (BY SIMILARITY).
 CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
 DOMAIN (BY SIMILARITY).
 CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
 EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
 FORM (BY SIMILARITY).
 CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
 SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

DR EMBL: AF083067; A021874.1;
 DR MGD; MGI:1933833; Nr94.

DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001336; EGF_1.
 DR Pfam: PR00008; EGF_1.
 DR PRINTS: PR00009; EGFTEG.
 DR SMART: SM00181; EGF_1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF-2; FALSE NEG.
 KW Growth factor; EGF-like domain; Glycoprotein; Transmembrane;
 KW Multigene family; Alternative splicing.
 FT CHAIN 1 115
 FT PRO-NEUREGULIN-4, MEMBRANE-BOUND FORM.
 FT NEUREGULIN-4.
 FT DOMAIN 1 62
 FT TRANSMEM 63 83
 FT DOMAIN 84 115
 FT DOMAIN 5 46
 FT DISULFID 9 23
 FT DISULFID 17 34
 FT DISULFID 36 45
 FT CARBOHYD 39 39
 FT CARBOHYD 60 60
 SQ SEQUENCE 115 AA; 12743 MW; 989A1E376F857849 CRC64;

Query Match 39.7%; Score 110; DB 1; Length 115;
 Best Local Similarity 42.2%; Pred. No. 1.2e-06;
 Matches 19; Conservative 8; Mismatches 16; Indels 2; Gaps 1;

OY 1 HEPGDRDLAYCNDGECVETLTGSHKH-CRCKEGYGRCDQ 45
 DB 5 HEPGDRHRSFCLNGICIVTPIRS--PFCRCIENTYARCEE 47

RESULT 6
 SMDF_HUMAN STANDARD: PRT; 296 AA.
 ID 015491;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuregulin-1, sensory and motor neuron-derived factor isoform.
 GN NRGI OR HGL OR NDF OR HRGA OR GGF OR SMDF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain stem, and Cerebellum;
 RX MEDLINE=95301541; PubMed=7782315;
 RA Ho W.-H., Armanini M.P., Nijlens A., Phillips H.S., Osheroff P.L.;
 RT Sensory and motor neuron-derived factor. A novel heregulin variant
 highly expressed in sensory and motor neurons.
 RL J. Biol. Chem. 270:14523-14532(1995).
 CC -1- FUNCTION: THE ISOFORM SMDF MAY PLAY A ROLE IN MOTOR AND SENSORY
 NEURON DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: SECRETED. MAY POSSESS AN INTERNAL UNCLEAVED
 SIGNAL SEQUENCE.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 10 ISOFORMS OF NRGI ARE PRODUCED BY
 ALTERNATIVE SPLICING. EXCEPT FOR SMDF THEY ARE IN ENTRY AC 002297.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NERVOUS SYSTEM: SPINAL CORD MOTOR
 NEURONS, DORSAL ROOT GANGLION NEURONS, AND BRAIN. PREDOMINANT
 ISOFORM EXPRESSED IN SENSORY AND MOTOR NEURONS. NOT DETECTED IN
 ADULT HEART, PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY, AND
 PANCREAS. NOT EXPRESSED IN FETAL LUNG, LIVER, AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN DEVELOPING SPINAL MOTOR
 NEURONS AND IN DEVELOPING CRANIAL NERVE NUCLEI. EXPRESSION IS
 MAINTAINED ONLY IN BOTH ADULT MOTOR NEURONS AND DORSAL ROOT
 GANGLION NEURONS.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.

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EMBL: L41837; AAC1764.1; -
HSSP: 012784; 1HRE.
MIM: 142445; -
InterPro: IPR000561; EGF-like.
SMART: SM00181; EGF, 1.
PROSITE: PS00022; EGF, 1.
PROSITE: PS01186; EGF_2; FALSE_NEG.
Growth factor; EGF-like domain; Transmembrane; Multigene family;
Alternative splicing.
TRANSMEM 76 100 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
DOMAIN 58 91 C17-RICH.
DOMAIN 211 232 SER/THR-RICH.
DOMAIN 233 277 EGF-LIKE.
DISULFID 237 251 BY SIMILARITY.
DISULFID 245 265 BY SIMILARITY.
DISULFID 267 276 BY SIMILARITY.
SEQUENCE 296 AA: 31685 MW: 80417432177EB02 CRC64:

Query Match 37.7%; Score 104.5; DB 1; Length 296;
Best Local Similarity 31.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

1 HRPKPRDLAVCLNDGCEVETLTGSHKH-CRCKEGYGVRCQDF 47
233 HLYKAEKERTCVNGSCFVYKLSNPSRYLCKCPNEFTDRCONYV 280

RESULT 7
NRG2_MOUSE STANDARD; PRT: 756 AA.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) (Contains: Neuregulin-2 (NRG-2) (Divergent of neuregulin 1) (DON-1)).

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

SEQUENCE FROM N.A. (ISOFORMS NRG2-5; NRG2-10 AND NRG2-16A).
STRAIN-C57BL/6; TISSUE-Brain.

MEDLINE-9731398; PubMed-9168115.

Caraway K.L., Ilt, Weber J.L., Unger M.J., Ledesma J., Yu N.,

Gassmann M., Lai C.,

"Neuregulin-2, a new ligand of ErbB3/ErbB4-receptor tyrosine

kinases".

Nature 387:512-516(1997).

SEQUENCE OF 150-756 FROM N.A. (ISOFORMS DON-1M AND DON-1S).

TISSUE-Choroid plexus.

MEDLINE-97342638; PubMed-9199335;

Bushfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,

Woolf E.A., Comrack C.A., Dussault B.J., Woolf J., Goodheart A.D.,

Gearing D.P.;

"Characterization of a neuregulin-related gene, Don-1, that is highly

expressed in restricted regions of the cerebellum and hippocampus".

Mol. Cell. Biol. 17:4007-4014(1997).

-1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE

RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORREPTORS,

ACTIVATING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND

HETERODIMERIZATION WITH THE EGF RECEPTOR.

-1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS

A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE

CC

CC

MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
-1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: DON-1M, DON-1S/NRG2-5,
NRG2-10 AND NRG2-16A (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
SPLICING.

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ID NRGL1.RAT STANDARD: PRT: 662 AA.
AC P43322; P43323; P43324; P43325; P43326; P43327; P43328;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pro-neuregulin-1 precursor (Pro-NRG1) [Contains: Neuregulin-1 (Neu
DE differentiation factor) (Heregulin) (HRG) (Acetylcholine receptor
DE inducing activity) (ARIA) (Sensory and motor neuron-derived factor)
DE (Glia growth factor)].
OS NG1 OR NDP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-FIBROBLAST;
RX MEDLINE-9415863; PubMed-7509448;
RA Wen D., Sugas S.V., Karunakaran D., Liu N., Cupples R.L., Luo Y.,
RA Janssen A.M., Ben-Baruch N., Trollinger D.B., Jacobsen V.L.,
RA Meng S.-Y., Lu H.S., Hu S., Chang D., Yang W., Yanigahara D.,
RA Koski R.A., Yarden Y.
RT Structural and functional aspects of the multiplicity of Neu
RT differentiation factors.*;
RL Mol. Cell. Biol. 14:1909-1919(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA2C/NDF44), AND PARTIAL SEQUENCE.
RC TISSUE-FIBROBLAST;
RX MEDLINE-92257596; PubMed-1349853;
RA Men D., Pales E., Cupples R., Sugas S.V., Bacus S.S., Luo Y.,
RA Trall G., Hu S., Silbiger S.M., Levy R.B., Koski R.A., Lu H.S.,
RA Yarden Y.
RT New differentiation factor: a transmembrane glycoprotein containing
RT an EGF domain and an immunoglobulin homology unit.*;
RL Cell 69:559-572(1992).
RN [3]
RP SEQUENCE OF 14-36.
RX MEDLINE-92208945; PubMed-1348215;
RA Pales E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
RA Levy R.B., Yarden Y.
RT Isolation of the neu/HER-2 stimulatory ligand: a 44 kd glycoprotein
RT that induces differentiation of mammary tumor cells.*;
RL Cell 69:205-216(1992).
RN [4]
RP REGULATION OF PROCESSING (ISOFORM ALPHA2C/NDF44).
RX MEDLINE-99069430; PubMed-9852099;
RA Liu X., Huang H., Cao L., Wen D., Liu N., Graham R.M., Zhou M.,
RT Release of the neuregulin functional polypeptide requires its
RT cytoplasmic tail.*;
RL J. Biol. Chem. 273:34335-34340(1998).
RN [5]
RP INTERACTION WITH LIMK1.
RX MEDLINE-98352096; PubMed-9685409;
RA Wang J.T., Frenzel K.E., Wen D., Falls D.L.;
RT Transmembrane neuregulin interact with Lim kinase 1, a cytoplasmic
RT protein kinase implicated in development of visuospatial cognition*;
RL J. Biol. Chem. 273:20525-20534(1998).
RN [6]
RP FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE
RP RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,
RP RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
RP ACTIVATION OF THE ERBB RECEPTORS. THE MULTIPLE ISOFORMS PERFORM
RP DIVERSE FUNCTIONS SUCH AS INDUCING GROWTH AND DIFFERENTIATION OF
RP EPITHELIAL, GLIAL, NEURONAL, AND SKELETAL MUSCLE CELLS; INDUCING
RP EXPRESSION OF ACETYLCHOLINE RECEPTOR IN SYNAPTIC VESICLES DURING
RP THE FORMATION OF THE NEUROMUSCULAR JUNCTION; STIMULATING
RP LOBULOVULAR BUDDING AND MILK PRODUCTION IN THE MAMMARY GLAND
RP AND INDUCING DIFFERENTIATION OF MAMMARY TUMOR CELLS; STIMULATING
RP SCHWANN CELL PROLIFERATION; IMPLICATION IN THE DEVELOPMENT OF THE
RP MYOCARDIUM SUCH AS TRABECULATION OF THE DEVELOPING HEART (BY
RP SIMILARITY).
RN [7]
RP SUBUNIT: THE CYTOPLASMIC DOMAIN INTERACTS WITH THE LIM DOMAIN
RP REGION OF LIMK1.
RN [8]
RP SUBCELLULAR LOCATION: EXISTS AS A TYPE I MEMBRANE PROTEIN AND AS A

CC PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE MEMBRANE-
CC BOUND FORM DOES NOT SEEM TO BE ACTIVE.
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 8 ISOFORMS: ALPHA2A/NDF38,
CC ALPHA2B/NDF19, ALPHA2C/NDF44, BETA1, BETA2/NDP40, BETA2A/NDP22,
CC BETA3/NDP4 AND BETA4/NDP42A (SHOWN HERE); ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. MOST TISSUES CONTAIN ALPHA2A
CC AND ALPHA2B ISOFORMS. ALPHA2A AND BETA2 ARE THE PREDOMINANT FORMS
CC IN MESENCHYMAL AND NONNEURONAL ORGANS. BETA1 IS ENRICHED IN BRAIN
CC AND SPINAL CORD, BUT NOT IN MUSCLE AND HEART. ALPHA2C IS HIGHLY
CC EXPRESSED IN SPINAL CORD, MODERATELY IN LUNG, BRAIN, OVARY, AND
CC STOMACH. IN LOW AMOUNTS IN THE KIDNEY, SKIN AND HEART AND NOT
CC DETECTED IN THE LIVER, SPLEEN, AND PLACENTA.
CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF
CC TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
CC DIMERIZATION.
CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
CC DOMAIN.
CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
CC FORM.
CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
CC -----
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CC EMBL: 002316; AAA19941.1; -
CC EMBL: 002317; AAA19942.1; -
CC EMBL: 002318; AAA19943.1; -
CC EMBL: 002319; AAA19944.1; -
CC EMBL: 002320; AAA19945.1; -
CC EMBL: 002321; AAA19946.1; -
CC EMBL: 002322; AAA19947.1; -
CC EMBL: 002323; AAA19948.1; -
CC EMBL: 002324; AAA19949.1; -
CC EMBL: M92430; -; NOT_ANNOTATED_CDS.
CC HSSP: Q12784; 1HRE.
CC InterPro: IPR000561; EGF-like.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR002154; Neuregulin.
CC Pfam: PF00008; EGF_1.
CC Pfam: PF00047; Ig_1.
CC Pfam: PF02158; Neuregulin; 1.
CC PRINTS: PRO1089; NEUREGULIN.
CC SMART: SM00181; EGF; 1.
CC SMART: SM00408; IGC2; 1.
CC PROSITE: PS00022; EGF_1; 1.
CC PROSITE: PS01186; EGF_2; FALSE_NEG.
CC Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
CC Transmembrane; Multigene family; Alternative splicing.
CC PROPEP
CC 1 13
CC CHAIN 14 662 PRO-NEUREGULIN-1, MEMBRANE-BOUND FORM.
CC 14 264 NEUREGULIN-1.
CC TRANSMEM 266 288 EXTRACELLULAR (POTENTIAL).
CC DOMAIN 289 662 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CC DOMAIN 50 119 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 165 177 IG-LIKE C2-TYPE DOMAIN.
CC DOMAIN 178 222 SER/THR-RICH.
CC DISULFID 57 112 EGF-LIKE.
CC DISULFID 157 196 BY SIMILARITY.
CC DISULFID 182 196 BY SIMILARITY.
CC DISULFID 190 210 BY SIMILARITY.

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 FT LACILSLICLACIACVAVFVDFKIFEDSPHLDGIGODPR
 FT STVDPTALSAWPEYVSEPIPSLESKEVYVDDSSIV
 FT PSRPILOSLYNIILVGLVMSAPSPSPSPSPSPSPSPSP
 FT ATEPNIQIAPKLS (TN ISOFORM BETA1A, ISOFORM
 FT BETA2A AND ISOFORM BETA2B)
 FT MISSING (IN ISOFORM BETA2A AND ISOFORM
 FT BETA2B).
 FT VSMPTTPARKSPVDFHTP -> HTPPTSLLAGKSVLRVS
 FT (IN ISOFORM BETA2B).
 FT VARSPLIC 388 405
 FT VARSPLIC 406 602
 FT VARSPLIC 602 AA: 67453 MW: 41830CE56CE5D346 CRC64;
 FT MISSING (IN ISOFORM BETA2B).
 FT SEQUENCE 602 AA: 67453 MW: 41830CE56CE5D346 CRC64;
 SO SEQUENCE 602 AA: 67453 MW: 41830CE56CE5D346 CRC64;
 Query Match 35.6%; Score 98.5; DB 1; Length 602;
 Best Local Similarity 33.3%; Pred. No. 0.00014;
 Matches 16; Conservative 11; Mismatches 20; Indels 1; Gaps 1;
 QY 1 HFKCRDKDLAVGNDCEVIFLTSNKH-CRCKEGYGVRCDFL 47
 Db 137 HLTGCDIKAKAFVNGCECTWADLPNPRILCRCPNEFTGDCONTY 184
 RESULT 10
 NRG2_HUMAN STANDARD; PRT; 850 AA.
 ID NRG2_HUMAN
 AC 014511;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
 DE (Neural and thymus-derived activator for ERBB kinases) (NTAK)
 DE (Divergent of neuregulin 1) (DON-1)].
 GN NRG2 OR NTAK.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid:9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Neuroblastoma;
 RX MEDLINE=98006334; PubMed=9348101;
 RA Higashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N.,
 RA Nakagawa T., Miyagawa J., Matsushita N., Nagatsu T., Taniguchi N.,
 RA Ishiguro H.;
 RT A novel brain-derived member of the epidermal growth factor family
 RT that interacts with erbB and ErbB4.
 RL J. Biochem. 122:675-680(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS DON-1B AND DON-1R).
 RC TISSUE=Fetal brain;
 RX MEDLINE=97342638; PubMed=9199335;
 RA Busfield S.J., Michnick D.A., Chickering T.W., Revett T.L., Ma J.,
 RA Woolf E.A., Comrak C.A., Dussault B.J., Woolf J., Goodheart A.D.J.,
 RA Geating D.P.;
 RT Characterization of a neuregulin-related gene, Don-1, that is highly
 RT expressed in restricted regions of the cerebellum and hippocampus.
 RL Mol. Cell. Biol. 17:4007-4014(1997).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).
 RC TISSUE=Lung, and fetal brain;
 RX MEDLINE=97393636; PubMed=10369162;
 RA Ring H.Z., Chang H., Guilbot A., Brice A., Leguern E., Francke U.;
 RT The human neuregulin 2 (NRG2) gene: cloning, mapping and evaluation
 RT as a candidate for the autosomal recessive form of Charcot-Marie-Tooth
 RT disease linked to 5q.
 RL Hum. Genet. 104:326-332(1999).
 CC -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE
 CC RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,
 CC RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
 CC ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE
 CC HETEROOLIGOMERIZATION WITH THE EGF RECEPTOR.
 CC HETEROOLIGOMERIZATION WITH THE EGF RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
 CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE

CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 8 ISOFORMS; 1 (SHOWN HERE), 2, 3, 4, 5, 6,
 CC DON-1B AND DON-1R. ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: RESTRICTED TO THE CEREBELLUM IN THE ADULT.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
 CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
 CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
 CC DIMERIZATION (BY SIMILARITY).
 CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
 CC DOMAIN (BY SIMILARITY).
 CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
 CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
 CC FORM (BY SIMILARITY).
 CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
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 DR HSSP: Q12784; IHRE.
 DR MIM: 603818; .
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR002134; Neuregulin.
 DR Pfam: PF00008; EGF; 1.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF02158; Neuregulin; 2.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS00222; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR Growth factor: EGF-like domain; Glycoprotein; Multigene family; Alternative splicing.
 DR Transmembrane: Multigene family; Alternative splicing.
 FT PROPEP 1 111
 FT CHAIN 112 650
 FT CHAIN 112 404
 FT DOMAIN 112 404
 FT TRANSSEM 406 426
 FT DOMAIN 427 850
 FT DOMAIN 250 318
 FT DOMAIN 330 340
 FT DOMAIN 341 382
 FT DOMAIN 10 13
 FT DOMAIN 20 30
 FT DOMAIN 33 47
 FT DOMAIN 87 90
 FT DOMAIN 721 727
 FT DISULFID 257 311
 FT DISULFID 345 359
 FT DISULFID 353 370
 FT DISULFID 372 381
 FT CARBOHYD 52 52
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 FT CARBOHYD 147 147
 FT CARBOHYD 278 278
 FT CARBOHYD 346 346
 FT VARSPLIC 1 233
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 FT SEQUENCE 850 AA: 91678 MW: 7124C089435FD24 CRC64:
 Query Match 32.5% Score 90; DB 1; Length 850;

Best Local Similarity 34.9%; Pred. No. 0.002;
 Matches 15; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
 Oy 1 HFKPCRDALAYCNDGCEVETLTGSHKRCCKEGYQVRC 43
 Db 341 HARKCNETAKSYCVNGCYVYIEGI--NQLSCKCPNGFGQRC 381
 RESULT 11
 NR02_RAT
 ID NR02_RAT STANDARD; PRT; 868 AA.
 AC O35569; O35570; O35571; O35572; O35073;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2)
 DE (Neural and thymus-derived activator for ERBB kinases) (NTAK)].
 GN NRG2 OR NTAK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN SEQUENCE FROM N.A., SEQUENCE OF 128-162, AND ALTERNATIVE SPLICING.
 RX MEDLINE-98006324; PubMed-9348101.
 RA Higashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N.,
 RA Nakagawa T., Miyagawa J., Matsushita N., Negatsu T., Taniguchi N.,
 RA Ishiguro H.;
 RT "A novel brain-derived member of the epidermal growth factor family
 RT that interacts with ERBB3 and ERBB4."
 RL J. Biochem. 122:675-680(1997).
 RP (2)
 RP SEQUENCE OF 109-868 FROM N.A. (ISOFORMS NRG2-ALPHA AND NRG2-BETA).
 RC TISSUE=Cerebellum;
 RX MEDLINE-97311397; PubMed-9168114;
 RA Chang H., Riese D.J. II, Gilbert W., Stern D.F., McManus U.J.;
 RT "Ligands for ErbB-family receptors encoded by a neuregulin-like
 RT gene".
 RL Nature 387:509-512(1997).
 CC -1- FUNCTION: DIRECT LIGAND FOR ERBB3 AND ERBB4 TYROSINE KINASE
 CC RECEPTORS. CONCOMITANTLY RECRUITS ERBB1 AND ERBB2 CORECEPTORS,
 CC RESULTING IN LIGAND-STIMULATED TYROSINE PHOSPHORYLATION AND
 CC ACTIVATION OF THE ERBB RECEPTORS. MAY ALSO PROMOTE THE
 CC HETERODIMERIZATION WITH THE EGF RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: EXISTS AS AN TYPE I MEMBRANE PROTEIN AND AS
 CC A PROTEOLYTICALLY RELEASED SOLUBLE GROWTH FACTOR FORM. THE
 CC MEMBRANE-BOUND FORM DOES NOT SEEM TO BE ACTIVE (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 7 ISOFORMS; NTAK-ALPHA1 (SHOWN
 CC HERE), NTAK-ALPHA2, NTAK-ALPHA2B/NTAK-ALPHA2-1P, NTAK-BETA, NTAK-
 CC GAMMA, NRG2-ALPHA AND NRG2-BETA; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING. THE ALPHA-TYPE AND BETA-TYPE DIFFER IN THE EGF-LIKE
 CC DOMAIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST PARTS OF THE BRAIN,
 CC ESPECIALLY THE OLFACTORY BULB AND CEREBELLUM WHERE IT LOCALIZES IN
 CC GRANULE AND PURKINJE CELLS. IN THE HIPPOCAMPUS, FOUND IN THE
 CC GRANULE CELLS OF THE DENTATE GYRUS. IN THE BASAL FOREBRAIN, FOUND
 CC IN THE CHOLINERGIC CELLS. IN THE HINDBRAIN, WEALTHY DETECTABLE IN
 CC THE MOTOR TRIGEMINAL NUCLEUS. NOT DETECTED IN THE HYPOTHALAMUS.
 CC ALSO FOUND IN THE LIVER AND IN THE THYMUS. NOT DETECTED IN HEART,
 CC ADRENAL GLAND, OR TESTIS.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED IN THE BRAIN OF
 CC ELL.5 EMBRYOS WHERE IT IS FOUND IN THE TELENEPHALON, BUT NOT IN
 CC THE HINDBRAIN. NOT FOUND IN THE HEART. IN THE ADULT, FOUND IN
 CC BRAIN AND THYMUS.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION
 CC OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE
 CC PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN
 CC DIMERIZATION (BY SIMILARITY).
 CC -1- DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE
 CC DOMAIN (BY SIMILARITY).
 CC -1- PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE
 CC EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR
 CC FORM (BY SIMILARITY).

CC -1- PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTEOLYTIC CLEAVAGE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
 CC -----
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 CC EMBL: AB001576; BAA23348.1; -
 CC HSSP: Q12784; 1HRE
 CC InterPro: IPR000561; EGF-1-like
 CC InterPro: IPR003006; Iq_MHC
 CC InterPro: IPR003598; Iq_C2
 CC InterPro: IPR002154; Neuregulin
 CC Pfam: PF00008; EGF_1
 CC Pfam: PF02158; Neuregulin; 2
 CC SMART: SM00181; EGF; 1
 CC SMART: SM00408; IgC2; 1
 CC PROSITE: PS00022; EGF_1; 1
 CC PROSITE: PS01186; EGF_2; 1
 CC Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
 CC Transmembrane; Multigene family; Alternative splicing.
 CC PROPEP 1 127
 CC CHAIN 128 868 PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM.
 CC CHAIN 128 428 NEUREGULIN-2.
 CC TRANSMEM 430 450 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 451 868 INTERNAL SIGNAL SEQUENCE (POTENTIAL).
 CC DOMAIN 265 334 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 345 356 Iq-LIKE C2-TYPE DOMAIN.
 CC DOMAIN 357 398 SER/THR-RICH.
 CC DOMAIN 22 32 EGF-LIKE.
 CC DOMAIN 35 45 POLY-SER.
 CC DOMAIN 56 59 POLY-SER.
 CC DOMAIN 103 106 POLY-THR.
 CC DOMAIN 739 745 POLY-ALA.
 CC DISULFID 273 327 BY SIMILARITY.
 CC DISULFID 361 375 BY SIMILARITY.
 CC DISULFID 369 386 BY SIMILARITY.
 CC DISULFID 388 397 BY SIMILARITY.
 CC CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 362 362 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 1 108 MISSING (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 220 222 PLY -> PEE (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 388 388 C -> G (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 389 388 MISSING (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 390 412 NEGFORCLEKPLRLYMPDPQ -> VGYTDRCOOFAMV
 CC VARSPLIC 390 421 NGS (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 390 421 NEGFORCLEKPLRLYMPDPQ -> VGYTDRCOOFAMV
 CC VARSPLIC 414 421 DRCOOFAMVNSK (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 414 439 MISSING (IN ISOFORM NRG2-BETA).
 CC VARSPLIC 414 439 ISOFORM NRG2-BETA).
 CC VARSPLIC 414 439 HGFELKAEELYLQRRVLTIGCYA -> SYLMDTPGTV
 CC VARSPLIC 440 868 SSSQWSTSPSTLDN (IN ISOFORM NRG2-ALPHA).
 CC VARSPLIC 117 868 MISSING (IN ISOFORM NRG2-ALPHA).
 CC VARSPLIC 117 868 S -> F (IN REF. 2).
 CC VARSPLIC 724 724 R -> H (IN REF. 2).
 CC VARSPLIC 724 724 R -> H (IN REF. 2).
 CC VARSPLIC 868 AA; 93776 MW; 3C7DAD94DBE64DE2 CRC64;

Query Match 32.5%; Score 90; DB 1; Length 868;
 Best Local Similarity 34.9%; Pred. No. 0.002;
 Matches 15; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
 OY 1 HFRCPDKDLAYCLNGCECVIETLNSHRCRCKEYGVRC 43
 DB 357 HARKNETAKSYGVNGCVYISGI--NOLSCRCPNCFQRC 397
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 EREG_HUMAN STANDARD: PRT; 169 AA.
 AC 014944;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2001 (Rel. 39, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Epregrulin precursor.
 GN EREG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid-9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE-COLORECTAL adenocarcinoma;
 RX MEDLINE-97479200; PubMed-9337852;
 RA Toyoda H., Komurasaki T., Uchida D., Morimoto S.;
 RT Distribution of mRNA for human epregrulin, a differentially expressed
 RT member of the epidermal growth factor family.*;
 RL Blochem. J. 326:69-75(1997).
 CC -1- FUNCTION: MAY BE A MEDIATOR OF LOCALIZED CELL PROLIFERATION. AS A
 CC MITOGEN IT MAY STIMULATE CELL PROLIFERATION AND/OR ANGIOGENESIS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM);
 CC -1- EXTRACELLULAR (MATURE FORM).
 CC -1- TISSUE SPECIFICITY: IN NORMAL ADULTS EXPRESSED PREDOMINANTLY IN THE
 CC PLACENTA AND PERIPHERAL BLOOD LEUCOCYTES. HIGH LEVELS WERE DETECTED
 CC IN CARCINOMAS OF THE BLADDER, LUNG, KIDNEY AND COLON.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
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 CC MIM: 602061; -
 CC DR InterPro: IPR000561; EGF-1-like.
 CC DR InterPro: IPR001336; EGF_1.
 CC DR PRINTS: PR00009; EGFTEF.
 CC DR SMART: SM00181; EGF; 1
 CC DR PROSITE: PS01186; EGF_2; 1.
 CC Growth factor; Mitogen; Glycoprotein; EGF-like domain; Transmembrane.
 CC SIGNAL 1 29
 CC PROPEP 30 59 POTENTIAL.
 CC CHAIN 60 108 EPIREGULIN.
 CC PROPEP 109 169 REMOVED IN MATURE FORM (BY SIMILARITY).
 CC DOMAIN 60 119 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 120 140 POTENTIAL.
 CC DOMAIN 141 169 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 145 152 ANG/LYS-RICH (BASIC).
 CC CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 64 104 EGF-LIKE.
 CC DOMAIN 68 81 BY SIMILARITY.
 CC DISULFID 76 92 BY SIMILARITY.
 CC DISULFID 94 103 BY SIMILARITY.
 CC SEQUENCE 169 AA; 19044 MW; 17F3926ADB2BDEE CRC64;
 Query Match 32.3%; Score 89.5; DB 1; Length 169;
 Best Local Similarity 40.5%; Pred. No. 0.0005;


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FT DOMAIN 178 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 218 EGF-LIKE 6.
FT DOMAIN 255 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 293 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 333 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 372 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 412 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 452 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 490 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 528 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 566 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 603 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 641 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 678 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 716 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 753 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 791 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 827 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 869 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 907 EGF-LIKE 24, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 945 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 983 EGF-LIKE 26, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1021 EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1059 EGF-LIKE 28, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1097 EGF-LIKE 29, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1145 EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1183 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1221 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1265 EGF-LIKE 33, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1307 EGF-LIKE 34, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1346 EGF-LIKE 35, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1387 EGF-LIKE 36, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1426 EGF-LIKE 37, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1465 EGF-LIKE 38, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1503 EGF-LIKE 39, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1541 EGF-LIKE 40, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1579 EGF-LIKE 41, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1617 EGF-LIKE 42, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1655 EGF-LIKE 43, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1693 EGF-LIKE 44, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1731 EGF-LIKE 45, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1769 EGF-LIKE 46, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1807 EGF-LIKE 47, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1845 EGF-LIKE 48, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1883 EGF-LIKE 49, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1921 EGF-LIKE 50, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1959 EGF-LIKE 51, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1997 EGF-LIKE 52, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2035 EGF-LIKE 53, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2073 EGF-LIKE 54, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2111 EGF-LIKE 55, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2149 EGF-LIKE 56, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2187 EGF-LIKE 57, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2225 EGF-LIKE 58, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2263 EGF-LIKE 59, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2301 EGF-LIKE 60, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2339 EGF-LIKE 61, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2377 EGF-LIKE 62, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2415 EGF-LIKE 63, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2453 EGF-LIKE 64, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2491 EGF-LIKE 65, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2529 EGF-LIKE 66, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2567 EGF-LIKE 67, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2605 EGF-LIKE 68, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2643 EGF-LIKE 69, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2681 EGF-LIKE 70, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2719 EGF-LIKE 71, CALCIUM-BINDING (POTENTIAL).
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FT DOMAIN 2795 EGF-LIKE 73, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2833 EGF-LIKE 74, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2871 EGF-LIKE 75, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2909 EGF-LIKE 76, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2947 EGF-LIKE 77, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 2985 EGF-LIKE 78, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3023 EGF-LIKE 79, CALCIUM-BINDING (POTENTIAL).
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FT DOMAIN 3213 EGF-LIKE 84, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3251 EGF-LIKE 85, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3289 EGF-LIKE 86, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3327 EGF-LIKE 87, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3365 EGF-LIKE 88, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3403 EGF-LIKE 89, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3441 EGF-LIKE 90, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3479 EGF-LIKE 91, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3517 EGF-LIKE 92, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3555 EGF-LIKE 93, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3593 EGF-LIKE 94, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3631 EGF-LIKE 95, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3669 EGF-LIKE 96, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3707 EGF-LIKE 97, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3745 EGF-LIKE 98, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3783 EGF-LIKE 99, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3821 EGF-LIKE 100, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3859 EGF-LIKE 101, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3897 EGF-LIKE 102, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3935 EGF-LIKE 103, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 3973 EGF-LIKE 104, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4011 EGF-LIKE 105, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4049 EGF-LIKE 106, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4087 EGF-LIKE 107, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4125 EGF-LIKE 108, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4163 EGF-LIKE 109, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4201 EGF-LIKE 110, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4239 EGF-LIKE 111, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4277 EGF-LIKE 112, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4315 EGF-LIKE 113, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4353 EGF-LIKE 114, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4391 EGF-LIKE 115, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4429 EGF-LIKE 116, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 4467 EGF-LIKE 117, CALCIUM-BINDING (POTENTIAL).

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Query Match 30.0% Score 83; DB 1; Length 2531;
Best Local Similarity 41.7% Pred. No. 0.037;
Matches 15; Conservative 4; Mismatches 13; Indels 4; Gaps 1;

OY 9 DLAVCLNDGECFVETLGSNHRCKRCKEGYGVRCDD 44
DB 1064 DSAPCKNGRCW---QNTQVHCRCRSGMTGVNCD 1095

RESULT 15
BTC_MOUSE STANDARD; PRT; 177 AA.
AC 005928;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Betacellulin precursor (BTC).
GN BTC OR BCM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 32-54; 64-71 AND 75-111.
RC TISSUE=Pancreas;
RX MEDLINE=93206093; PubMed=8456283;

```

RA Shing Y., Christofori G., Hanahan D., Ono Y., Sasada R.,
 RA Igarashi K., Folkman J.;
 RT "Betacellulin: a mitogen from pancreatic beta cell tumors";
 RL Science 259:1604-1607(1993).
 CC -1- FUNCTION: POTENT MITOGEN FOR RETINAL PIGMENT EPITHELIAL CELLS
 CC AND VASCULAR SMOOTH MUSCLE CELLS. THE EFFECTS OF BETACELLULIN
 CC ARE PROBABLY MEDIATED BY THE EGF RECEPTOR AND OTHER RELATED
 CC RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PRECURSOR FORM);
 CC EXTRACELLULAR (MATURE FORM).
 CC -1- TISSUE SPECIFICITY: FOUND IN SEVERAL MOUSE TISSUES INCLUDING
 CC KIDNEY, UTERUS AND LIVER AS WELL AS IN BETA TUMOR CELL LINE AND
 CC MCF-7 CELLS. IT IS NOT DETECTED IN THE BRAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 DR EMBL: L08394, AAA40511.1, -;
 DR PIR: A37408, A37408.
 DR HSSP: P01135, 3TGF.
 DR MCD: MGI:99439, Btc.
 DR InterPro: IPR000561, EGF_1like.
 DR InterPro: IPR001336, EGF_1.
 DR Pfam: PF00008, EGF_1.
 DR PRINTS: PRO0009, EGFTGF.
 DR SMART: SM00181, EGF, 1.
 DR SMART: SM00001, EGF_1like, 1.
 DR PROSITE: PS00022, EGF_1, 1.
 DR PROSITE: PS01186, EGF_2, 1.
 KW Growth factor; Mitogen; Glycoprotein; EGF-like domain; Transmembrane;
 KW Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 111
 FT PROPEP 112 177
 FT DOMAIN 32 118
 FT TRANSMEM 119 139
 FT DOMAIN 140 177
 FT DOMAIN 65 105
 FT DOMAIN 146 153
 FT DISULFID 69 82
 FT DISULFID 77 93
 FT DISULFID 95 104
 FT CARBOHYD 34 34
 FT CARBOHYD 42 42
 FT CARBOHYD 52 52
 SQ SEQUENCE 177 AA; 19664 MW; 066BB34F0E13F82B CRC64;
 Query Match 29.8%; Score 82.5; DB 1; Length 177;
 Best Local Similarity 39.18; Pred. No. 0.0036;
 Matches 18; Conservative 9; Mismatches 14; Indels 5; Gaps 3;

OY 1 HFKPCRDKLAVCLNDEC-FVIEITLGSNKHCRCKEGYGVGRCDQ 45
 || | : ||: | ||: | | : || | ||: |
 Db 65 HFSRCPRQYKHYCIH-GRCRFVVDGTPS--CICEKGYFGARCR 106
 || | : ||: | ||: | | : || | ||: |

Search completed: November 7, 2002, 10:00:02
 Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:08 ; Search time 19 Seconds

(without alignments)
237.695 Million cell updates/sec

Title: US-09-480-977-4

Sequence: 1 HFKRCRDLAYCLNDGECF.....SHKRCRKGYGVRCDQPL 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: PIR71:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	100.0	713	2 T44447	neuregulin-3 (limp
2	113.5	41.0	125	2 I38405	neu differentiatio
3	113.5	41.0	462	2 I38404	neu differentiatio
4	113.5	40.3	640	2 A43273	heregulin precurs
5	111.5	40.3	639	2 I61719	neu differentiatio
6	105.5	38.1	125	2 S62676	heregulin isoform
7	104.5	37.7	175	2 I38408	neu differentiatio
8	104.5	37.7	241	2 S32359	glial growth facto
9	104.5	37.7	241	2 D43273	heregulin precurs
10	104.5	37.7	296	2 A56443	senory/motor neur
11	104.5	37.7	422	2 S32357	glial growth facto
12	104.5	37.7	637	2 C43273	heregulin precurs
13	104.5	37.7	645	2 B43273	heregulin, splice
14	102.5	37.0	230	2 A56210	neu differentiatio
15	102.5	37.0	636	2 I61718	neu differentiatio
16	102.5	37.0	662	2 I61722	neu differentiatio
17	98.5	35.6	602	2 A45769	acetylcholine rece
18	92.5	33.4	2180	2 T29764	hypothetical prote
19	90	32.5	850	2 JC5700	Erbb kinase activa
20	90	32.5	860	2 JC5702	Erbb kinase activa
21	90	32.5	868	2 JC5701	growth factor - ra
22	85	30.7	80	1 BGVXSF	jagged protein pre
23	84.5	30.5	1220	2 A56136	epilegulin - rat
24	83	30.0	46	2 JT0747	epilegulin precurs
25	83	30.0	162	2 S68401	Notch homolog Motc
26	83	30.0	861	2 A48825	Notch-1 protein -
27	83	30.0	2531	2 A46019	betacellulin precu
28	82.5	29.8	177	2 A37408	growth factor - my
29	82	29.6	85	1 BGVZM1	

30	82	29.6	230	2 A44074	probable EGF-like
31	82	29.6	264	2 T22380	hypothetical prote
32	80.5	28.1	178	2 JC1467	betacellulin precu
33	80	28.9	907	2 T27317	hypothetical prote
34	79.5	28.7	140	1 MWV29	growth factor - va
35	79.5	28.7	140	2 T30766	growth factor - va
36	79.5	28.7	142	1 MWV23C	growth factor - va
37	79.5	28.7	159	1 WPRF1	transforming growt
38	79.5	28.7	159	1 S27195	transforming growt
39	79.5	28.7	159	2 I57497	transforming growt
40	79	28.5	2531	2 S18188	notch protein homo
41	78	28.2	1207	1 EGHU	epidermal growth f
42	77.5	28.0	722	2 I48324	DETRA-like 1 - mou
43	77.5	28.0	2352	2 T30201	Notch homolog prot
44	76.5	27.6	1372	2 T25933	hypothetical prote
45	76	27.4	482	2 JC5092	E-selectin - pig

ALIGNMENTS

RESULT 1
T44447
neuregulin-3 (Imported) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T44447
R:Zhang, D.; Sliwkowski, M.X.; Mark, M.; Franke, G.; Akita, R.; Sun, Y.; Hillan, K.
Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997
A:Title: Neuregulin-3 (NRG3): A novel neural tissue-enriched protein that binds and
A:Reference number: 222773; MVID:97420720
A:Accession: T44447
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-713 <ZHA>
A:Cross-references: EMBL:AF010130; NID:g2429163; PIDN:AAB70914.1; PID:g2429164
C:Genetics:
A:Gene: NRG3

Query Match 100.0%; Score 277; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 4.7e-24;
Matches 47; Conservative 0; Mismatches ~0; Indels 0; Gaps 0;

QY 1 HFKRCRDLAYCLNDGECFVITLGSNHCRCRKGYGVRCDQPL 47
DB 288 HFKRCRDLAYCLNDGECFVITLGSNHCRCRKGYGVRCDQPL 334

RESULT 2
I38405
neu differentiatation factor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I38405
R:Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, M.; Cell. Biol. 14, 1909-1919, 1994
A:Title: Structural and functional aspects of the multiplicity of Neu differentiat.
A:Reference number: A56210; MVID:94158863
A:Accession: I38405
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <RES>
A:Cross-references: EMBL:U02327; NID:g408404; PIDN:AAA19952.1; PID:g408405

Query Match 41.0%; Score 113.5; DB 2; Length 125;
Best Local Similarity 34.8%; Pred. No. 5.1e-06;
Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;
QY 1 HFKRCRDLAYCLNDGECFVITLGSNHCRCRKGYGVRCDQ 45
DB 56 HFKRCRDLAYCLNDGECFVITLGSNHCRCRKGYGVRCDQ 101

Query Match 38.1%; Score 105.5; DB 2; Length 125;
 Best Local Similarity 32.6%; Pred. No. 4.2e-05;
 Matches 15; Conservative 14; Mismatches 16; Indels 1; Gaps 1;
 Oy 1 HFKPCRDKLAVCLNDGCEVFYETLTGSHKH-CRCKEGYGVRCDFL 45
 Db 75 HLYVCAKEKTEFCVNGGECFVWDLSPNSRYLCKCPNEFTGDRCONVY 120

RESULT 7
 138408
 neu differentiation factor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
 C:Accession: 138408
 R:Men, D.; Suggs, S.V.; Karunakaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
 Mol. Cell. Biol. 14, 1909-1919, 1994
 A:Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
 A:Reference number: A56210; MUID:94158863
 A:Accession: 138408
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-175 <RES>
 A:Cross-references: EMBL:U02330; NID:9408410; PIDN:AA19955.1; PID:9408411
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 F:116-155/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 175;
 Best Local Similarity 31.2%; Pred. No. 7.3e-05;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;
 Oy 1 HFKPCRDKLAVCLNDGCEVFYETLTGSHKH-CRCKEGYGVRCDFL 47
 Db 112 HLYVCAKEKTEFCVNGGECFVWDLSPNSRYLCKCPNEFTGDRCONVY 159

RESULT 8
 532359
 glial growth factor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 11-Jan-2000
 C:Accession: 532359
 R:Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Her
 les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M.
 Nature 362, 312-318, 1993
 A:Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the r
 A:Reference number: S32357; MUID:93205115
 A:Accession: 532359
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-241 <MAR>
 A:Cross-references: GB:L12259; NID:9289413; PIDN:AA30540.1; PID:9289414
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 F:182-221/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 241;
 Best Local Similarity 31.2%; Pred. No. 9.6e-05;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;
 Oy 1 HFKPCRDKLAVCLNDGCEVFYETLTGSHKH-CRCKEGYGVRCDFL 47
 Db 178 HLYVCAKEKTEFCVNGGECFVWDLSPNSRYLCKCPNEFTGDRCONVY 225

RESULT 9
 D43273
 heregulin precursor, splice form beta-3 - human
 N:Alternate names: glial growth factor HRG-beta-3; heregulin
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000
 C:Accession: D43273; S32358
 R:Holmes, W.E.; Sliwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansu
 Science 256, 1205-1210, 1992

A:Title: Identification of heregulin, a specific activator of p185(erbB2).
 A:Reference number: A43273; MUID:92271253
 A:Accession: D43273
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptua
 A:Molecule type: mRNA
 A:Residues: 1-241 <HOL>
 R:Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.
 les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield,
 Nature 362, 312-318, 1993
 A:Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in
 A:Reference number: S32357; MUID:93205115
 A:Accession: 532358
 A:Molecule type: mRNA
 A:Residues: 1-241 <MAR>
 A:Cross-references: GB:L12261; NID:9292049; PIDN:AA59358.1; PID:9292050
 C:Genetics:
 A:Gene: GDB:HGL; GGF
 A:Cross-references: GDB:132656; OMIM:142445
 A:Map position: 8p22-8p11
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: alternative splicing
 F:182-221/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 241;
 Best Local Similarity 31.2%; Pred. No. 9.6e-05;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;
 Oy 1 HFKPCRDKLAVCLNDGCEVFYETLTGSHKH-CRCKEGYGVRCDFL 47
 Db 178 HLYVCAKEKTEFCVNGGECFVWDLSPNSRYLCKCPNEFTGDRCONVY 225

RESULT 10
 A56943
 sensory/motor neuron-derived factor - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 11-Jan-2000
 C:Accession: A56943
 R:Ho, W.H.; Armanini, M.P.; Nuljens, A.; Phillips, H.S.; Osheroff, P.L.
 J. Biol. Chem. 270, 14523-14532, 1995
 A:Title: Sensory and motor neuron-derived factor. A novel heregulin variant highly
 A:Reference number: A56943; MUID:95301541
 A:Accession: A56943
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-296 <HOA>
 A:Cross-references: GB:L41827; NID:9862422; PIDN:AA41764.1; PID:9862423
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 F:237-276/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 296;
 Best Local Similarity 31.2%; Pred. No. 0.00011;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;
 Oy 1 HFKPCRDKLAVCLNDGCEVFYETLTGSHKH-CRCKEGYGVRCDFL 47
 Db 233 HLYVCAKEKTEFCVNGGECFVWDLSPNSRYLCKCPNEFTGDRCONVY 280

RESULT 11
 S32357
 glial growth factor - human
 C:Species: Homo sapiens (man)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2000
 C:Accession: S32357
 R:Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.
 les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield,
 Nature 362, 312-318, 1993
 A:Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in
 A:Reference number: S32357; MUID:93205115
 A:Accession: S32357
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-422 <MAP>
 A:Cross-references: GB:112260; NID:9292047; PIDN:AA059622.1; PID:9292048
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 F:363-402/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 422;
 Best Local Similarity 31.2%; Pred. No. 0.00016;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

OY 1 HFRPCRDLDAYCLNDGCFVIEITLGSNKH-CRCKEGYGVRCDOFL 47
 DB 359 HLVKCAEKETFCVNGGCEFMVKDLSNPSRYLCKCPNEFTGDRCONYV 406

RESULT 12

heregulin precursor, splice form beta-2 - human

C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text_change 17-Nov-2000
 C:Accession: C43273; 138407
 R:Holmes, W.E.; Sliwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansui
 Science 256, 1205-1210, 1992
 A:Title: Identification of heregulin, a specific activator of p185(erbB2).
 A:Reference number: A43273; MUID:92271253

A:Accession: C43273
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
 A:Molecule type: mRNA
 A:Residues: 1-637 <HOLD>
 R:Men, D.; Sugge, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
 Mol. Cell. Biol. 14, 1909-1919, 1994
 A:Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
 A:Reference number: A56210; MUID:94158863
 A:Accession: 138407
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 119-406 <RES>
 A:Cross-references: EMBL:002329; NID:9408408; PIDN:AA19954.1; PID:9408409

C:Genetics:

A:Gene: GDB:HGL
 A:Cross-references: GDB:132656; OMIM:142445
 A:Map position: 8p22-8p11
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: alternative splicing
 F:182-221/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 637;
 Best Local Similarity 31.2%; Pred. No. 0.00022;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

OY 1 HFRPCRDLDAYCLNDGCFVIEITLGSNKH-CRCKEGYGVRCDOFL 47
 DB 178 HLVKCAEKETFCVNGGCEFMVKDLSNPSRYLCKCPNEFTGDRCONYV 225

RESULT 13

heregulin, splice form beta 1 - human

C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text_change 17-Nov-2000
 C:Accession: B43273; 138406
 R:Holmes, W.E.; Sliwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansui
 Science 256, 1205-1210, 1992
 A:Title: Identification of heregulin, a specific activator of p185(erbB2).
 A:Reference number: A43273; MUID:92271253

A:Accession: B43273

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
 A:Molecule type: mRNA
 A:Residues: 1-645 <HOLD>

R:Men, D.; Sugge, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
 Mol. Cell. Biol. 14, 1909-1919, 1994
 A:Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
 A:Reference number: A56210; MUID:94158863

A:Accession: 138406

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 'A', 95-418, 'F', 420-645 <RES>
 A:Cross-references: EMBL:002328; NID:9408406; PIDN:AA19953.1; PID:9408407

C:Genetics:

A:Gene: GDB:HGL
 A:Cross-references: GDB:132656; OMIM:142445
 A:Map position: 8p22-8p11
 C:Superfamily: unassigned EGF-related proteins; EGF homology
 C:Keywords: alternative splicing
 F:182-221/Domain: EGF homology <EGF>

Query Match 37.7%; Score 104.5; DB 2; Length 645;
 Best Local Similarity 31.2%; Pred. No. 0.00022;
 Matches 15; Conservative 14; Mismatches 18; Indels 1; Gaps 1;

OY 1 HFRPCRDLDAYCLNDGCFVIEITLGSNKH-CRCKEGYGVRCDOFL 47
 DB 178 HLVKCAEKETFCVNGGCEFMVKDLSNPSRYLCKCPNEFTGDRCONYV 225

RESULT 14

neu differentiation factor - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Jul-1996 #sequence, revision 02-Jul-1996 #text_change 26-May-2000
 C:Accession: A56210
 R:Men, D.; Sugge, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.
 Mol. Cell. Biol. 14, 1909-1919, 1994
 A:Title: Structural and functional aspects of the multiplicity of Neu differentiation
 A:Reference number: A56210; MUID:94158863
 A:Accession: A56210

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-230 <RES>
 A:Cross-references: EMBL:002315; NID:9408380; PIDN:AA19940.1; PID:9408381
 C:Superfamily: unassigned EGF-related proteins; EGF homology

Query Match 37.0%; Score 102.5; DB 2; Length 230;
 Best Local Similarity 31.2%; Pred. No. 0.00016;
 Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

OY 1 HFRPCRDLDAYCLNDGCFVIEITLGSNKH-CRCKEGYGVRCDOFL 47
 DB 167 HLVKCAEKETFCVNGGCEFTVADLSNPSRYLCKCPNEFTGDRCONYV 214

RESULT 15

neu differentiation factor - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-May-1998 #sequence, revision 29-May-1998 #text_change 17-Nov-2000
 C:Accession: I61718; I61721; I61720
 R:Men, D.; Sugge, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.
 Mol. Cell. Biol. 14, 1909-1919, 1994
 A:Title: Structural and functional aspects of the multiplicity of Neu differentiation
 A:Reference number: A56210; MUID:94158863
 A:Accession: I61718

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-636 <RES>

A:Cross-references: EMBL:002318; NID:9408386; PIDN:AA19943.1; PID:9408387

A:Accession: I61721

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298, 386, 'V', 388, 'TR', 391 <RES>
 A:Cross-references: EMBL:002320; NID:9408390; PIDN:AA19945.1; PID:9408391
 C:Superfamily: unassigned EGF-related proteins; EGF homology

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us-09-480-977-4.rpr

Page 5

F:182-221/Domain: EGF homology <EGF>

Query Match 37.08; Score 102.5; DB 2; Length 636;

Best Local Similarity 31.28; Pred. No. 0.00038;

Matches 15; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 1 HFKRNDKDLAYCLNDGECFVIELTIGSHKH-CRCKEGYGVRCDOFL 47

Db 178 HLIKCAEKETFCVNGGCEFTVKDLSPNSRYLCPCNEFTGDRQNTV 225

Search completed: November 7, 2002, 10:00:27
Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:04 ; Search time 30 Seconds
(without alignments)
174.016 Million cell updates/sec

Title: US-09-480-977-4

Sequence: 1 HRPGRDNDLAVCLNDSECF.....SHKRCRKGQGVRCDFL 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	100.0	47	20	AAW97622
2	277	100.0	157	20	AAW05451
3	277	100.0	360	20	AAW97621
4	277	100.0	362	20	AAW97620
5	277	100.0	696	20	AAW97619
6	277	100.0	713	20	AAW97617
7	277	100.0	720	20	AAW05452
8	277	100.0	720	20	AAW97616
9	116.5	42.1	52	17	AAW05182
10	116.5	42.1	52	21	AAW12602
11	116.5	42.1	52	21	AAW69983

12	113.5	41.0	52	17	AAW05184	Neu differentiation
13	113.5	41.0	63	15	AAW46918	EGFL2. AAR46918;
14	113.5	41.0	63	15	AAW55659	EGFL2. AAR55659;
15	113.5	41.0	63	16	AAW67250	Human epidermal 11
16	113.5	41.0	63	17	AAW09363	EGFL2. Not specif
17	113.5	41.0	63	17	AAW96076	Epidermal growth f
18	113.5	41.0	63	17	AAW87461	Epidermal growth f
19	113.5	41.0	66	21	AAW36702	EGF-like domain of
20	113.5	41.0	83	15	AAW46922	EGFL6. AAR46922;
21	113.5	41.0	83	15	AAW55663	EGFL6. AAR55663;
22	113.5	41.0	83	16	AAW67254	Human epidermal 11
23	113.5	41.0	83	17	AAW09367	EGFL6. Not specif
24	113.5	41.0	83	17	AAW96080	Epidermal growth f
25	113.5	41.0	83	17	AAW87465	Epidermal growth f
26	113.5	41.0	88	15	AAW46921	EGFL5. AAR46921;
27	113.5	41.0	88	15	AAW55662	EGFL5. AAR55662;
28	113.5	41.0	88	16	AAW67253	Human epidermal 11
29	113.5	41.0	88	17	AAW09366	EGFL5. Not specif
30	113.5	41.0	88	17	AAW96079	Epidermal growth f
31	113.5	41.0	88	17	AAW87464	Epidermal growth f
32	113.5	41.0	101	22	AAW67933	Human NRG1 protein
33	113.5	41.0	101	22	AAW67933	Human NRG1 protein
34	113.5	41.0	125	16	AAW68564	Human NDF protein
35	113.5	41.0	125	22	AAW67928	Human NDF- α 1p43 c
36	113.5	41.0	125	22	AAW67966	Human NRG1 gene Ne
37	113.5	41.0	125	13	AAW28537	Human NRG1 gene Ne
38	113.5	41.0	263	15	AAW46896	GGF2BBP2. CDS prote
39	113.5	41.0	263	15	AAW55689	GGF2BBP2. Bos tau
40	113.5	41.0	263	16	AAW67217	GGF2BBP2. Bos tau
41	113.5	41.0	263	17	AAW09360	Putative bovine gl
42	113.5	41.0	280	15	AAW46915	Bovine neurotrophin
43	113.5	41.0	280	15	AAW55656	GGF2BBP2. Bos tau
44	113.5	41.0	280	16	AAW67244	GGF2BBP2. Bos tau
45	113.5	41.0	280	17	AAW09369	Bovine glial cell

ALIGNMENTS

RESULT 1
AAW97622
ID AAW97622 standard; Protein: 47 AA.
AC AAW97622;
XX 10-MAY-1999 (first entry)
DT
XX
XX Human neurotrophin related ligand NRG3 EGF-like domain.
DE
XX
XX Neurotrophin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor;
KW signal transduction; nervous system disorder; neurodegeneration;
RW neuropathy; therapy; diagnosis; epidermal growth factor; EGF;
KW immunoadhesin.
XX
XX Homo sapiens.
XX
XX W09902681-A1.
XX
XX 21-JAN-1999.
XX
XX 30-JUN-1998; 98WO-US13411.
XX
XX 24-JUL-1997; 97US-0899437.
XX
XX 09-JUL-1997; 97US-0052019.
XX
XX (GETH) GENENTECH INC.
XX
XX Godowski PJ, Mark MR, Zhang D;
XX
XX WPI: 1999-120882/10.
XX
XX New isolated neurotrophin related ligand-3 - used to develop products
XX for treating nervous system disorders, e.g. stroke, ischemia,
XX

PT Infection, malignancy, Alzheimer's disease or Down's syndrome
XX
PS Claim 30; Page 64; 101pp; English.

XX This is the epidermal growth factor (EGF)-like domain of human
XX neuroligin related ligand NR3 (see also AAW97618), a novel member of
XX the EGF-like family of protein ligands that binds to the ErbB4
XX receptor and activates ErbB4 receptor tyrosine phosphorylation.
XX The EGF-1 like domain of NR3 is distinct from the EGF-like domains
XX of NR3 and NR2. The invention provides human and murine
XX polypeptides (see also AAW97617) that have at least 75% homology to
XX the NR3 EGF-like domain, as well as expression vectors, host cells
XX and methods for the recombinant production of novel NR3s. The
XX NR3 polypeptides and polynucleotides and can be used to enhance
XX the survival, proliferation or differentiation of cells having the
XX ErbB4 receptor in vivo and in vitro. They can be used to prevent
XX or treat damage to a nerve or damage to other NR3-expressing or
XX NR3-responsive cells, e.g. brain, heart, or kidney cells. In
XX particular, they can be used to treat diseases which involve neural
XX cell growth such as demyelination, or damage or loss of glial cells
XX (e.g. multiple sclerosis). They can be used to treat patients whose
XX nervous system has been damaged by e.g. trauma, surgery, stroke,
XX ischemia, infection, metabolic disease, nutritional deficiency,
XX malignancy, or toxic agents. NR3 can also be used to treat
XX motor neuron disorders such as amyotrophic lateral sclerosis (Lou
XX Gehrig's disease), Bell's palsy, conditions involving spinal
XX muscular atrophy or paralysis, neurodegenerative disorders such as
XX Alzheimer's disease, Parkinson's disease, epilepsy, multiple
XX sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
XX and Meniere's disease. They can also be used to treat neuropathies
XX associated with systemic disease including post-polio syndrome,
XX hereditary neuropathies including Charcot-Marie-Tooth disease,
XX Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
XX disease, metachromatic leukodystrophy, Fabry's disease and
XX Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
XX smooth muscle, such as muscular dystrophy or diseases caused by
XX skeletal or smooth muscle wasting. The products can also be used
XX for detection, diagnosis, for the production of transgenic or
XX knockout animals or for drug screening. A claimed immunoadhesin
XX comprises the human NR3 EGF-like domain fused to an immunoglobulin
XX sequence.

SO Sequence 47 AA;

Query Match 100.0%; Score 277; DB 20; Length 47;
Best Local Similarity 100.0%; Pred. No. 2,5e-21;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDLDAYCINDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
DB 1 HFKPCRDLDAYCINDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47

RESULT 2
AAV05451
ID AAV05451 standard; Protein; 157 AA.

XX AAV05451;

XX 06-JUN-1999 (first entry)

XX Human heregulin-like factor sequence.

XX Human heregulin-like factor; HLF; cell growth regulator; diagnosis;
XX neural system disorder; cancer.

XX Homo sapiens.

XX MO9857989-A1.

XX 23-DEC-1998.

XX 16-JUN-1998; 98MO-US12403.

60/09/99
61/08/01

XX 17-JUN-1997; 9705-0049942.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (GEOU) UNIV GEORGETOWN.
XX H1421 MM, King CR, Ruben SM, Young P;
XX WPI; 1999-095327/08.
XX N-PSDB; AAX36423.
XX New isolated heregulin-like factor - used to develop products for
XX the diagnosis and treatment of disorders involving regulation of
XX cell growth, particularly cancers
XX
XX Claim 17; Page 86-87; 118pp; English.

XX This sequence is the human heregulin-like factor (HLF) of the
XX invention. The HLF is involved in the regulation of cell growth.
XX Detection of different levels of expression of the HLF gene can be used
XX for the diagnosis of disorders, e.g. in the neural system. In
XX particular, detection of different levels of HLF gene expression in cells
XX or body fluid of an individual can be used for diagnosing cancer. The
XX products can also be used in the treatment of disorders involving
XX abnormal levels of HLF activity.

SO Sequence 157 AA;

Query Match 100.0%; Score 277; DB 20; Length 157;
Best Local Similarity 100.0%; Pred. No. 7,6e-21;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDLDAYCINDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
DB 31 HFKPCRDLDAYCINDGECFVETLTGSHKRCRCKEGYGVRCDOFL 77

RESULT 3

ID AAW97621
ID AAW97621 standard; Protein; 360 AA.

XX AAW97621;

XX 10-MAY-1999 (first entry)

XX Human heregulin related ligand NR3 extracellular domain.

XX Neuroligin related ligand; NR3; hNR3B1; human; ErbB4 receptor;
XX signal transduction; nervous system disorder; neurodegeneration;
XX neuropathy; therapy; diagnosis.

XX Homo sapiens.

XX MO9902681-A1.

XX 21-JAN-1999.

XX 30-JUN-1998; 98MO-US13411.

XX 24-JUL-1997; 9705-0899437.

XX 09-JUL-1997; 9705-0052019.

XX (GETH) GENENTECH INC.

XX Godowski PJ, Mark MR, Zhang D;

XX WPI; 1999-120882/10.

XX New isolated heregulin related ligand-3 - used to develop products
XX for treating nervous system disorders, e.g. stroke, ischemia,
XX infection, malignancy, Alzheimer's disease or Down's syndrome

XX Claim 5(a); Page 69-70; 101pp; English.

XX This is the extracellular domain (ECD, aa1-360 of human neueregulin
 CC related ligand NRG3 (see also AAM97618), a novel member of the
 CC epidermal growth factor (EGF)-like family of protein ligands. NRG3
 CC binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor,
 CC activates ErbB4 receptor tyrosine phosphorylation. The invention
 CC provides human and murine polypeptides (see also AAM97617) that have
 CC at least 75% homology to the NRG3 ECD, as well as expression vectors,
 CC host cells and methods for the recombinant production of novel
 CC NRG3s. The NRG3 polypeptides and polynucleotides and can be used to
 CC enhance the survival, proliferation or differentiation of cells
 CC having the ErbB4 receptor in vivo and in vitro. They can be used to
 CC prevent or treat damage to a nerve or damage to other NRG3-expressing
 CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In
 CC particular, they can be used to treat diseases which involve neural
 CC cell growth such as demyelination, or damage or loss of glial cells
 CC (e.g. multiple sclerosis). They can be used to treat patients whose
 CC nervous system has been damaged by e.g. trauma, surgery, stroke,
 CC ischaemia, infection, metabolic disease, nutritional deficiency,
 CC malignancy, or toxic agents. NRG3 can also be used to treat
 CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou
 CC Gehrig's disease), Bell's palsy, conditions involving spinal
 CC muscular atrophy or paralysis, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple
 CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
 CC and Meniere's disease. They can also be used to treat neuropathies
 CC associated with systemic disease including post-polio syndrome,
 CC hereditary neuropathies including Charcot-Marie-Tooth disease,
 CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
 CC disease, metachromatic leukodystrophy, Fabry's disease and
 CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
 CC smooth muscle, such as muscular dystrophy or diseases caused by
 CC skeletal or smooth muscle wasting. The products can also be used
 CC for detection, diagnosis, for the production of transgenic or
 CC knockout animals or for drug screening.

SO Sequence 360 AA:

Query Match 100.0%; Score 277; DB 20; Length 360;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDKLAVCLNDGECFVETLTGSHKRCRCKEGYGVRCDFL 47
 ||||||||||||||||||||||||||||||||||||||||||||
 DB 286 HFKPCRDKLAVCLNDGECFVETLTGSHKRCRCKEGYGVRCDFL 332

RESULT 4

ID AAM97620 standard; Protein: 362 AA.

AC AAM97620;

DT 10-MAY-1999 (first entry)

DE Mouse neueregulin related ligand NRG3 extracellular domain.

KM Neueregulin related ligand; NRG3; mouse; ErbB4 receptor;

KW signal transduction; nervous system disorder; neurodegeneration;

XX neuropathy; therapy; diagnosis.

OS Mus sp.

PN WO9902681-A1.

PD 21-JAN-1999.

PF 30-JUN-1998; 98WO-0513411.

PR 24-JUL-1997; 97US-0899437.

PA 09-JUL-1997; 97US-0052019.

(GETH) GENENTECH INC.

XX Godowski PJ, Mark MR, Zhang D;
 PI WPI: 1999-120882/10.
 XX
 PT New isolated neueregulin related ligand-3 - used to develop products
 PT for treating nervous system disorders, e.g. stroke, ischaemia,
 PT infection, malignancy, Alzheimer's disease or Down's syndrome
 PS Claim 5(a): Page 62-63; 101pp; English.

XX This is the extracellular domain (ECD, aa1-362) of murine neueregulin
 CC related ligand NRG3 (see also AAM97617), a novel member of the
 CC epidermal growth factor (EGF)-like family of protein ligands. NRG3
 CC binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor,
 CC activates ErbB4 receptor tyrosine phosphorylation. The invention
 CC provides human and murine polypeptides (see also AAM97618) that have
 CC at least 75% homology to the NRG3 ECD, as well as expression vectors,
 CC host cells and methods for the recombinant production of novel
 CC NRG3s. The NRG3 polypeptides and polynucleotides and can be used to
 CC enhance the survival, proliferation or differentiation of cells
 CC having the ErbB4 receptor in vivo and in vitro. They can be used to
 CC prevent or treat damage to a nerve or damage to other NRG3-expressing
 CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In
 CC particular, they can be used to treat diseases which involve neural
 CC cell growth such as demyelination, or damage or loss of glial cells
 CC (e.g. multiple sclerosis). They can be used to treat patients whose
 CC nervous system has been damaged by e.g. trauma, surgery, stroke,
 CC ischaemia, infection, metabolic disease, nutritional deficiency,
 CC malignancy, or toxic agents. NRG3 can also be used to treat
 CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou
 CC Gehrig's disease), Bell's palsy, conditions involving spinal
 CC muscular atrophy or paralysis, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple
 CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
 CC and Meniere's disease. They can also be used to treat neuropathies
 CC associated with systemic disease including post-polio syndrome,
 CC hereditary neuropathies including Charcot-Marie-Tooth disease,
 CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
 CC disease, metachromatic leukodystrophy, Fabry's disease and
 CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
 CC smooth muscle, such as muscular dystrophy or diseases caused by
 CC skeletal or smooth muscle wasting. The products can also be used
 CC for detection, diagnosis, for the production of transgenic or
 CC knockout animals or for drug screening.

SO Sequence 362 AA:

Query Match 100.0%; Score 277; DB 20; Length 362;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFKPCRDKLAVCLNDGECFVETLTGSHKRCRCKEGYGVRCDFL 47
 ||||||||||||||||||||||||||||||||||||||||||||
 DB 288 HFKPCRDKLAVCLNDGECFVETLTGSHKRCRCKEGYGVRCDFL 334

RESULT 5

ID AAM97619 standard; Protein: 696 AA.

AC AAM97619;

DT 10-MAY-1999 (first entry)

DE Human neueregulin related ligand NRG3 (splice variant).

KM Neueregulin related ligand; NRG3; human; ErbB4 receptor;

KW signal transduction; nervous system disorder; neurodegeneration;

XX neuropathy; therapy; diagnosis; splice variant.

OS Homo sapiens.

FH Key Location/Qualifiers
 FT 1..360
 FT Domain /note= "extracellular domain, specifically claimed in Claim 5(a)"
 FT Region 66..91
 FT /note= "hydrophobic region"
 FT Region 101..284
 FT /note= "mucin-like Ser/Thr-rich region, contains sites for O-linked glycosylation"
 FT Domain 285..354
 FT /note= "EGF-like domain"
 FT Domain 355..394
 FT /note= "transmembrane domain"
 PN MO9902681-A1.
 PD 21-JAN-1999.
 PR 30-JUN-1998; 98WO-US13411.
 PR 24-JUL-1997; 97US-0899437.
 PR 09-JUL-1997; 97US-0052019.
 PA (GETH) GENENTECH INC.
 PI Godowski PJ, Mark MR, Zhang D;
 DR WPI: 1999-120882/10.
 DR N-PDB: AAX06987.
 PT New isolated neuroguilin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischemia, infection, malignancy, Alzheimer's disease or Down's syndrome
 PS Example 1: Page 78-81; 101pp; English.
 XX This is the amino acid sequence of splice variant hNGR3B2 of human neuroguilin related ligand NRG3, a novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the ErbB2 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor tyrosine phosphorylation. The sequence was deduced from the nucleotide sequence of a cDNA clone (see AAX06989) from a foetal brain library. hNGR3B2 lacks amino acids 529-552 of hNGR3B1 (see AAM97617) but retains the EGF-like domain and is expected to exhibit biological activity. The invention provides human and murine NRG3 polypeptides (see AAM97617), expression vectors, host cells and methods for the recombinant production of NRG3s. The NRG3 polypeptides and polynucleotides and can be used to enhance the survival, proliferation or differentiation of cells having the ErbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-expressing particular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage or loss of glial cells (e.g. multiple sclerosis). They can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, Reissner's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease, and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of skeletal muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening.

XX Sequence 696 AA:
 SQ Query Match 100.0%; Score 277; DB 20; Length 696;
 Best Local Similarity 100.0%; Pred. No. 3e-20;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HRPCKRDKDIAYCLNDGECFVETLTGSHKRCRKGQVRCDFL 47
 DB 286 HRPCKRDKDIAYCLNDGECFVETLTGSHKRCRKGQVRCDFL 332
 RESULT 6
 AAM97617
 ID AAM97617 standard; Protein: 713 AA.
 AC AAM97617;
 DT 10-MAY-1999 (first entry)
 DE Mouse neuroguilin related ligand NRG3.
 KW Neuroguilin related ligand; NRG3; mouse; ErbB4 receptor;
 KW signal transduction; nervous system disorder; neurodegeneration;
 KW neuropathy; therapy; diagnosis.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT 1..362
 FT Domain /note= "extracellular domain, specifically claimed in Claim 5(a)"
 FT Region 66..91
 FT /note= "hydrophobic region"
 FT Region 105..286
 FT /note= "mucin-like Ser/Thr-rich region, contains sites for O-linked glycosylation"
 FT Domain 287..334
 FT /note= "EGF-like domain"
 FT Domain 353..385
 FT /note= "transmembrane domain"
 PN MO9902681-A1.
 PD 21-JAN-1999.
 PR 30-JUN-1998; 98WO-US13411.
 PR 24-JUL-1997; 97US-0899437.
 PR 09-JUL-1997; 97US-0052019.
 PA (GETH) GENENTECH INC.
 PI Godowski PJ, Mark MR, Zhang D;
 DR WPI: 1999-120882/10.
 DR N-PDB: AAX06987.
 PT New isolated neuroguilin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischemia, infection, malignancy, Alzheimer's disease or Down's syndrome
 PS Claim 5(b): Page 59-62; 101pp; English.
 XX This is the amino acid sequence of murine neuroguilin related ligand NRG3, a novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the ErbB2 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor tyrosine phosphorylation. The sequence was deduced from the nucleotide sequences of cDNA clones (see AAX06987) from a mouse brain library. The EGF-like domain of NRG3 is distinct from those of NRG1 or NRG2, and NRG3 displays receptor binding characteristics that are distinct from those of other neuroguilins. The invention provides

CC human and murine NRG3 polypeptides (see also AAW97618), expression
 CC vectors, host cells and methods for the recombinant production of
 CC NRG3s. The NRG3 polypeptides and polynucleotides and can be used to
 CC enhance the survival, proliferation or differentiation of cells
 CC having the ErbB4 receptor in vivo and in vitro. They can be used to
 CC prevent or treat damage to a nerve or damage to other NRG3-expressing
 CC or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In
 CC particular, they can be used to treat diseases which involve neural
 CC cell growth such as demyelination, or damage or loss of glial cells
 CC (e.g. multiple sclerosis). They can be used to treat patients whose
 CC nervous system has been damaged by e.g. trauma, surgery, stroke,
 CC leishmaniasis, infection, metabolic disease, nutritional deficiency,
 CC malignancy, or toxic agents. NRG3 can also be used to treat
 CC motor neuron disorders such as amyotrophic lateral sclerosis (Lou
 CC Gehrig's disease), Bell's palsy, conditions involving spinal
 CC muscular atrophy or paralysis, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, multiple
 CC sclerosis, Huntington's chorea, Down's syndrome, nerve deafness,
 CC and Meniere's disease. They can also be used to treat neuropathies
 CC associated with systemic disease including post-polio syndrome,
 CC hereditary neuropathies including Charcot-Marie-Tooth disease,
 CC Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's
 CC disease, metachromatic leukodystrophy, Fabry's disease and
 CC Dejerine-Sottas syndrome, to treat disease of skeletal muscle of
 CC smooth muscle, such as muscular dystrophy or diseases caused by
 CC skeletal or smooth muscle wasting. The products can also be used
 CC for detection, diagnosis, for the production of transgenic or
 CC knockout animals or for drug screening.

XX Sequence 713 AA:

Query Match 100.0%; Score 277; DB 20; Length 713;
 Best Local Similarity 100.0%; Pred. No. 3.1e-20;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HRRPCRDKLAVCLNDGECFVETLTGSHKRCRKGVCGRDQFL 47
 DB 286 HRRPCRDKLAVCLNDGECFVETLTGSHKRCRKGVCGRDQFL 334

RESULT 7
 ID AAY05452 standard; Protein; 720 AA.

XX AAY05452;

DT 06-JUL-1999 (first entry)

XX Human heterogulin-like factor sequence.

KW Human heterogulin-like factor; HLF; cell growth regulator; diagnosis;
 XX neural system disorder; cancer.

OS Homo sapiens.

XX MO9857989-A1.

PD 23-DEC-1998.

PF 16-JUN-1998; 98MO-US12403.

PR 17-JUN-1997; 97US-0049942.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (GEOT) UNIV GEORGETOWN.

XX Hljact MM, King CR, Ruben SM, Young P;

DR MPI; 1999-095327/08.

PT New isolated heterogulin-like factor - used to develop products for
 PT the diagnosis and treatment of disorders involving regulation of
 PT cell growth, particularly cancers

XX Disclosure: Page 97-99; 118pp; English.

XX This sequence is the human heterogulin-like factor (HLF) of the
 CC invention. The HLF is involved in the regulation of cell growth.
 CC Detection of different levels of expression of the HLF gene can be used
 CC for the diagnosis of disorders, e.g. in the neural system. In
 CC particular, detection of different levels of HLF gene expression in cells
 CC or body fluid of an individual can be used for diagnosing cancer. The
 CC products can also be used in the treatment of disorders involving
 CC abnormal levels of HLF activity.

XX Sequence 720 AA:

Query Match 100.0%; Score 277; DB 20; Length 720;
 Best Local Similarity 100.0%; Pred. No. 3.1e-20;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HRRPCRDKLAVCLNDGECFVETLTGSHKRCRKGVCGRDQFL 47
 DB 286 HRRPCRDKLAVCLNDGECFVETLTGSHKRCRKGVCGRDQFL 332

RESULT 8

ID AAW97618 standard; Protein; 720 AA.

XX AAW97618;

DT 10-MAY-1999 (first entry)

XX Human heterogulin related ligand NRG3.

KW Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor;
 XX signal transduction; nervous system disorder; neurodegeneration;
 KW neuropathy; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..360 /note="extracellular domain; specifically claimed
 FT in Claim 5(a)."

FT Region 66..91 /note="hydrophobic region"

FT Region 101..284 /note="mucin-like Ser/Thr-rich region, contains
 FT sites for O-linked glycosylation"

FT Domain 285..354 /note="EGF-like domain"

FT Domain 356..394 /note="transmembrane domain"

XX MO9902681-A1.

PD 21-JAN-1999.

PF 30-JUN-1998; 98MO-US13411.

PR 24-JUL-1997; 97US-0899437.

PR 09-JUL-1997; 97US-0052019.

XX (GETH) GENENTECH INC.

PA Godowski PJ, Mark MR, Zhang D;

DR MPI; 1999-120882/10.

DR N-PSDB; AAX06988.

PT New isolated neuregulin related ligand-3 - used to develop products
 PT for treating nervous system disorders, e.g. stroke, ischaemia,
 PT infection, malignancy, Alzheimer's disease or Down's syndrome

PS Claim 5(b); Page 66-69; 101pp; English.
XX

has the amino acid sequence of human neurotrophin related ligand NGF3, a novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB receptor tyrosine phosphorylation. The sequence was deduced from the nucleotide sequence of a cDNA clone (see AA065988) from a foetal brain library. The EGF-like domain of NGF3 is distinct from those of NGF1 or NGF2, and NGF3 displays receptor binding characteristics that are distinct from those of other neurotrophins. An alternatively spliced form of human NGF3 is provided in AA07619. The invention provides human and murine NGF3 polypeptides (see also AA07617), expression vectors, host cells and methods for the recombinant production of NGF3s. The NGF3 polypeptides and polynucleotides and can be used to enhance the survival, proliferation or differentiation of cells having the ErbB4 receptor *in vivo* and *in vitro*. They can be used to prevent or treat damage to a nerve or damage to other NGF3-expressing cells or NGF3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage or loss of glial cells (e.g. multiple sclerosis). They can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents. NGF3 can also be used to treat motor neuron disorders such as amphotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, Refsum's disease, abetalipoproteinaemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease and Djerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening.

SQ Sequence 720 AA;

Query Match	100.0%;	Score 277;	DB 20;	Length 720;
Best Local Similarity	100.0%;	Pred. No. 3.1e-20;		
Matches 47;	Conservative 0;	Mismatches 0;	Indels 0;	Score 277;

Dy I HFKPCRDRLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDFL 47
|||||
Db 286 HFKPCRDKLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDFL 332

RESULT 9
AAW05182
ID AAW05182 standard; peptide; 52 AA
XX

XX
PR 06-APR-1995; 95DS-0417640.
XX
PA (AMGE-) AMGEN INC.
XX
PI Ciranahan JF, Hara S, Lu HS, Mayer JP, Yoshinaga SK;
XX DR WPI; 1996-465022/46.
XX
PT Peptide(s) derived from neu differentiation factor/herregulin
PT proteins - specifically from epidermal growth factor-like domain,
XX stimulate proliferation of colon epithelial cells and Schwann cells
PS Claim 1, Page 27; 37pp; English.

the peptides AAW05182-7W05185 are based on new differentiation factor (NDF)/heparin alpha and beta form EGF-like domains in various combinations. The peptides maintain the survival and proliferation of Schwann cells and cause proliferation, growth and differentiation of colon epithelial cells. Accordingly, they are useful to treat (in vitro or in vivo) a disease or disorder of the colon (e.g. colitis or an ulcer) or of the nervous system (e.g. nerve damage caused by trauma).

Query Match	42.1%	Score 116.5	DB 17	Length 52
Best Local Similarity	33.3%	Pred. No. 4.7e-05		
Matches 16	Conservative 15	Mismatches 16	Indels 1	Cons 1

2. HLYKCAEKENTFCVNGGECFMVKDLSNPSRYLCKQPGFTGARCQNY 49

```

RESULT 10
AAB12602
ID      AAB12602 standard; peptide; 52 AA
XX

```

CC: The present invention describes a monoclonal antibody (I) deposited with
CC the American Type Culture Collection under accession number HB-12598.
CC. The antibodies are used in study and research with adult rat utricular

PR 10-AUG-1992; 92US-0927337.
 PR 25-SEP-1992; 92US-0951747.
 PR 01-DEC-1992; 92US-0984085.
 PR 29-JAN-1993; 93US-0011396.
 XX
 PA (CAMP-) CAMBRIDGE NEUROSCIENCE INC.
 XX
 PI Gwyne DI, Marchionni M, McBurney RN;
 XX
 DR WPI: 1994-065731/08.
 DR N-PSDB; AAQ58324.
 XX
 PT Glial growth factor DNA encoding numerous polypeptide factors
 PT used for inhibiting cell proliferation - for treating carcinoma
 PT and nervous disorders
 XX
 PS Disclosure; Fig 40; 178pp; English.
 XX
 CC The GGF coding segments include regions with EGF-like homology.
 CC These EGF-like domains can be required for the activation of
 CC mitogenesis in the binding reaction between GGF ligands contg.
 CC such domains and the erbB2 receptor. Pref. antiproliferative
 CC factors are those which lack these EGF-like domains.
 XX
 SQ Sequence 63 AA;
 OY 1 HFRPCRDNDLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCQD 45
 DB 2 HLVKCAEKERTFCVNGGECFVWKDLSNPSRYLCKQCPGTGARCTE 47
 XX
 RESULT 14
 ID AAR55659 standard; Protein; 63 AA.
 XX
 AC AAR55659;
 XX
 DT 28-JUL-1994 (first entry)
 XX
 DE EGFL2.
 XX
 KW Glial growth factor; GGF; heregulin; mitogenesis;
 KW Schwann cell; tumour; central nervous system;
 KW epidermal growth factor; EGF.
 XX
 PN W09400140-A.
 XX
 PD 06-JAN-1994.
 XX
 PF 29-JUN-1993; 93WO-US06228.
 XX
 PR 30-JUN-1992; 92US-0907138.
 PR 03-SEP-1992; 92US-0940389.
 PR 23-OCT-1992; 92US-0965173.
 PR 24-MAR-1993; 93US-0036555.
 XX
 PA (CAMP-) CAMBRIDGE NEUROSCIENCE;
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Chen MS, Goodearl A, Hiles I, Marchionni M, Minghetti L;
 PI Stroobant P, Waterfield M;
 XX
 DR WPI: 1994-025882/03.
 DR N-PSDB; AAQ62843.
 XX
 PT Glial mitogenic polypeptide factors - useful for stimulating
 PT glial cell mitogenesis and treating glial cell tumours
 XX
 PS Claim 53; Fig 39; 178pp; English.

XX
 CC EGFL1, EGFL2, EGFL3, EGFL4, EGFL5 and EGFL6 are used
 CC for the stimulation of glial cell mitogenesis in vivo
 CC and in vitro.
 XX
 SQ Sequence 63 AA;
 OY 1 HFRPCRDNDLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCQD 45
 DB 2 HLVKCAEKERTFCVNGGECFVWKDLSNPSRYLCKQCPGTGARCTE 47
 XX
 RESULT 15
 ID AAR67250 standard; Protein; 63 AA.
 XX
 AC AAR67250;
 XX
 DT 15-AUG-1995 (first entry)
 XX
 DE Human epidermal like growth factor 2 (EGFL2).
 XX
 KW Epidermal like growth factor 2; mammalian muscle cell treatment;
 KW skeletal; cardiac; smooth; acetylcholine receptor deficiency;
 KW EGFL2.
 XX
 OS Homo sapiens.
 XX
 PN W09426298-A.
 XX
 PD 24-NOV-1994.
 XX
 PF 06-MAY-1994; 94WO-US05083.
 XX
 PR 06-MAY-1993; 93US-0059022.
 PR 08-MAR-1994; 94US-0209204.
 XX
 PA (CAMP-) CAMBRIDGE NEUROSCIENCE.
 XX
 PI Gwyne DI, Marchionni M, Sklar R;
 XX
 DR WPI: 1995-006353/01.
 DR N-PSDB; AAQ74915.
 XX
 PT Treating mammalian muscle diseases and disorders - by admin. of
 PT GGF2 and other specified polypeptide(s) which bind the p15terbB2
 PT receptor.
 XX
 PS Claim 34; Pages 148-149; 241pp; English.
 XX
 CC AAQ74915 encodes AAR67250 human epidermal like growth factor 2 (EGFL2).
 CC The glial cell mitogenic activity of EGFL2 can be used to treat a
 CC variety of mammalian skeletal, cardiac and smooth muscle diseases,
 CC including acetylcholine receptor deficiency.
 XX
 SQ Sequence 63 AA;
 OY 1 HFRPCRDNDLAYCLNDGECFVETLTGSHKH-CRCKEGYGVRCQD 45
 DB 2 HLVKCAEKERTFCVNGGECFVWKDLSNPSRYLCKQCPGTGARCTE 47
 XX
 Query Match 41.0%; Score 113.5; DB 16; Length 63;
 Best Local Similarity 34.8%; Pred. No. 0.00011;
 Matches 16; Conservative 14; Mismatches 15; Indels 1; Gaps 1;

Search completed: November 7, 2002, 09:59:44
 Job time : 32 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 7, 2002, 09:59:49 ; Search time 13 seconds
(without alignments)
88,308 Million cell updates/sec

Title: US-09-480-977-4

Perfect score: 277
Sequence: 1 HFKCRKDLAYCLNDCGCF.....SHKCRCKEGYGVRCDFL 47

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2_6/prodata/1/laa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/laa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/laa/6C.COMB.pep:*
6: /cgn2_6/prodata/1/laa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	100.0	47	US-08-899-437-4	Sequence 4, Appl
2	277	100.0	47	US-08-899-437-8	Sequence 8, Appl
3	277	100.0	47	US-09-126-121-4	Sequence 4, Appl
4	277	100.0	47	US-09-126-121-8	Sequence 8, Appl
5	277	100.0	360	US-08-899-437-7	Sequence 7, Appl
6	277	100.0	360	US-09-126-121-7	Sequence 7, Appl
7	277	100.0	362	US-08-899-437-3	Sequence 3, Appl
8	277	100.0	362	US-09-126-121-3	Sequence 3, Appl
9	277	100.0	696	US-08-899-437-23	Sequence 23, Appl
10	277	100.0	696	US-09-126-121-23	Sequence 23, Appl
11	277	100.0	713	US-08-899-437-2	Sequence 2, Appl
12	277	100.0	713	US-09-126-121-2	Sequence 2, Appl
13	277	100.0	720	US-08-899-437-6	Sequence 6, Appl
14	277	100.0	720	US-09-126-121-6	Sequence 6, Appl
15	116.5	42.1	52	US-08-417-640A-1	Sequence 1, Appl
16	116.5	42.1	52	US-08-760-815-1	Sequence 1, Appl
17	116.5	42.1	52	US-08-761-038-1	Sequence 1, Appl
18	116.5	42.1	52	US-08-761-038-1	Sequence 1, Appl
19	113.5	41.0	49	US-08-899-437-14	Sequence 14, Appl
20	113.5	41.0	49	US-09-126-121-14	Sequence 14, Appl
21	113.5	41.0	50	US-08-753-007A-12	Sequence 12, Appl
22	113.5	41.0	50	US-09-398-496-12	Sequence 12, Appl
23	113.5	41.0	52	US-08-417-640A-3	Sequence 3, Appl
24	113.5	41.0	52	US-08-760-815-3	Sequence 3, Appl
25	113.5	41.0	52	US-08-761-038-3	Sequence 3, Appl
26	113.5	41.0	54	US-08-179-481-111	Sequence 11, Appl
27	113.5	41.0	63	US-08-341-018-62	Sequence 62, Appl

28	113.5	41.0	63	4	US-08-470-335-221	Sequence 221, App
29	113.5	41.0	63	4	US-08-470-339-221	Sequence 221, App
30	113.5	41.0	66	1	US-07-847-743B-10	Sequence 10, Appl
31	113.5	41.0	66	1	US-08-456-201-10	Sequence 10, Appl
32	113.5	41.0	66	2	US-08-456-201-10	Sequence 10, Appl
33	113.5	41.0	66	4	US-09-020-880-2	Sequence 2, Appl
34	113.5	41.0	66	5	PCT-US92-04295A-10	Sequence 10, Appl
35	113.5	41.0	83	3	US-08-341-018-70	Sequence 70, Appl
36	113.5	41.0	83	4	US-08-470-335-225	Sequence 225, App
37	113.5	41.0	88	4	US-08-470-339-225	Sequence 225, App
38	113.5	41.0	88	4	US-08-341-018-68	Sequence 68, Appl
39	113.5	41.0	88	4	US-08-470-335-224	Sequence 224, App
40	113.5	41.0	88	4	US-08-470-335-224	Sequence 224, App
41	113.5	41.0	95	1	US-07-847-743B-14	Sequence 14, Appl
42	113.5	41.0	95	1	US-08-456-201-14	Sequence 14, Appl
43	113.5	41.0	95	2	US-08-330-161-12	Sequence 12, Appl
44	113.5	41.0	95	2	US-08-456-241-14	Sequence 14, Appl
45	113.5	41.0	95	2	US-08-440-401-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-899-437-4
Sequence 4, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: NRG3 EGF-like domain/amino acid seq.
LOCATION: 1-47
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-4

Query Match 100.0%; Score 277; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 HFKCRKDLAYCLNDCGCFVETLTGSHKCRCKEGYGVRCDFL 47
|||||

DB 1 HRPCKRDLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47

RESULT 2
US-08-899-437-8

Sequence 8, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/899,437

FILING DATE: 24-Jul-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Conley, Delidre L.

REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1084R1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

FEATURE:

NAME/KEY: NR3 EGF-like domain/amino acid seq.

LOCATION: 1-47

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-08-899-437-8

Query Match 100.0%; Score 277; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HRPCKRDLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
DB 1 HRPCKRDLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47

RESULT 3
US-09-126-121-4

Sequence 4, Application US/09126121

Patent No. 6252051

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/126,121

FILING DATE: 30-Jul-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Conley, Delidre L.

REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1084R1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

FEATURE:

NAME/KEY: NR3 EGF-like domain/amino acid seq.

LOCATION: 1-47

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-126-121-4

Query Match 100.0%; Score 277; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HRPCKRDLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
DB 1 HRPCKRDLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47

RESULT 4
US-09-126-121-8

Sequence 8, Application US/09126121

Patent No. 6252051

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/126,121

FILING DATE: 30-Jul-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Conley, Delidre L.

REGISTRATION NUMBER: 36,487

REFERENCE/DOCKET NUMBER: P1084R1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-2066

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 47 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

FEATURE:
NAME/KEY: NRG3 EGF-like domain/amino acid seq.
LOCATION: 1-47
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-8

Query Match 100.0%; Score 277; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 47
DB 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 47

RESULT 5
US-08-899-437-7
Sequence 7, Application US/08899437
Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-2066

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

FEATURE:
NAME/KEY: NRG3 extracellular domain/amino acidseq
LOCATION: 1-360
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-7

Query Match 100.0%; Score 277; DB 3; Length 360;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 47
DB 286 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 332

RESULT 6
US-09-126-121-7
Sequence 7, Application US/09126121
Patent No. 6252051

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-9881
TELEFAX: 650/225-2066

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

FEATURE:
NAME/KEY: NRG3 extracellular domain/amino acidseq
LOCATION: 1-360
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-7

Query Match 100.0%; Score 277; DB 4; Length 360;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 47
DB 286 HFRPCRDKLAYCLNDGECFVETLTGSHKRCCKEGYGVRCDOFL 332

RESULT 7
US-08-899-437-3
Sequence 3, Application US/08899437
Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997

FEATURE:
NAME/KEY: NRG3 extracellular domain/amino acidseq
LOCATION: 1-360
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-7

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: mNRG3 extracellular domain amino acid seq
LOCATION: 1-362
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-3

Query Match: 100.0%; Score 277; DB 3; Length 362;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 47
Db 288 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 334

RESULT 8

US-09-126-121-3
Sequence 3, Application US/09126121
Patent No. 6252051

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

FEATURE:

NAME/KEY: mNRG3 extracellular domain amino acid seq
LOCATION: 1-362
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-3

Query Match: 100.0%; Score 277; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 47
Db 288 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 334

RESULT 9

US-08-899-437-23
Sequence 23, Application US/08899437
Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

FEATURE:

NAME/KEY: Human NRG3B2
LOCATION: 1-696
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-23

Query Match: 100.0%; Score 277; DB 3; Length 696;
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 47
Db 286 HFKCRDKDLAYCLNDECFVIEITLGSNHRCKRCKEGYGVRCDOFL 332

RESULT 10

US-09-126-121-23
Sequence 23, Application US/09126121
Patent No. 6252051

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Human NRG3B2
LOCATION: 1-696
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-23

Query Match 100.0%; Score 277; DB 4; Length 696;
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
|||||
DB 286 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 332

RESULT 11
US-08-899-437-2
Sequence 2, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
LOCATION: 1-713
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-2

Query Match 100.0%; Score 277; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
|||||
DB 286 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 334

RESULT 12
US-09-126-121-2
Sequence 2, Application US/09126121
Patent No. 6252051

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
LOCATION: 1-713
IDENTIFICATION METHOD:
OTHER INFORMATION:

US-09-126-121-2

Query Match 100.0%; Score 277; DB 4; Length 713;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 47
|||||
DB 286 HFRPCRDKLAYCLNDGECFVETLTGSHKRCRCKEGYGVRCDOFL 334

RESULT 13
US-08-899-437-6
Sequence 6, Application US/08899437
Patent No. 6131415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: hNRG3B1 amino acid sequence
LOCATION: 1-720
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-899-437-6
Query Match 100.0%; Score 277; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 2,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 HFKPCRDVLAYCLNDGECFYETLTGSHKRCRKEGYGVRCDOFL 47
DB 286 HFKPCRDVLAYCLNDGECFYETLTGSHKRCRKEGYGVRCDOFL 332
RESULT 14
US-09-126-121-6
Sequence 6, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Conley, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
NAME/KEY: hNRG3B1 amino acid sequence
LOCATION: 1-720
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-09-126-121-6
Query Match 100.0%; Score 277; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 2,1e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 HFKPCRDVLAYCLNDGECFYETLTGSHKRCRKEGYGVRCDOFL 47
DB 286 HFKPCRDVLAYCLNDGECFYETLTGSHKRCRKEGYGVRCDOFL 332
RESULT 15
US-08-417-640A-1
Sequence 1, Application US/08417640A
Patent No. 5670342
GENERAL INFORMATION:
APPLICANT: Carnahan, Josette F.
APPLICANT: Hara, Shinichi
APPLICANT: Lu, Hsiang S.
APPLICANT: Mayer, John P.
APPLICANT: Yoshinaga, Steven K.
TITLE OF INVENTION: NDF Peptides
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,640A
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mazza, Richard J.
REFERENCE/DOCKET NUMBER: A-310
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

